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 /organism: "unidentified"
 /feature: "32644"

BASE COUNT 166 a 80 c 86 g 139 t
 ORIGIN

alignment_scores:
 Quality: 782.00 Length: 157
 Ratio: 5.045 Gaps: 0
 Percent Similarity: 98.726 Percent Identity: 98.089

alignment_block:

US 09 479-862-1 x E17146 ..

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451 TTCACTGTCAGAAAGCAAGAC 471
  
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AUTHORS

Dias Neto, F., Garcia, C., and F. V. de Almeida, 1993, *Relatório*, M. P. Nogueira, M. A. da Silva, W. J. de Souza, M. A. de Bordin, S. Costa, F. F. Goldman, C. H. Carvalho, A. F. Matsumoto, A. R. de S. S. Simpson, D. H. Brunstein, A. de Oliveira, P. S. Bucher, P. J. Juncione, C. V. de O. Hare, M. J. Soares, F. Brentani, R. R. Reis, L. F. de Souza, S. L. and J. Simpson, A. J.

Shoquin sequencing of the human transcritome with 40K expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (1), 3491-3496 (2000)
20202663

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Brazil

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$$F_{\text{div}} = 155 \cdot 11 \cdot 2707(11)$$

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/CNPq Human Cancer Genome project. This entry can be seen in the following URL.

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VERSION BE979995.1 GI:18647511
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 5 (9): 791-906 (1995)
97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N 7190, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: MEST@nimh.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
basal ganglia tissue cDNA Library Preparation: M.B. Soares Lab
Clone distribution: Researchers may obtain BMAP cDNA clones from
RESEARCH GENETICS. It should be noted that: Beato Soares is
generating a small number of additional specialized non-redundant
arrays of BMAP cDNAs whose availability will be considered under
appropriate and limited collaborative arrangements the following
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EcoRI linker. Site 1: Not I; Site 2: Eco RI; The
NIH-BMAP_MSC_S1 library is a subtracted library derived
from BMAP_MSC-R. NIH-BMAP_MSC_N was made from mouse spinal
cord tissue. For a detailed description of the library
from which this clone was derived, please visit our web
site at brainest.ouk.owa.edu.
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seq_documentation_block:
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DEFINITION US0947989 Normalized rat E18897, Beato Soares Ratius sp. cDNA clone

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EST 25 JAN 1999

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 part of E7.5 embryos, extraembryonic part of E7.5 embryos
 and E12.5 female mesonephros/anad) and one newborn
 ovary cDNA library. Average insert size 1.5 kb. All
 source libraries are cloned unidirectionally with clonase
 3'-R4 primers. References include: (1) Genome wide
 expression profiling of mid-gestation placenta and embryo
 using a 15,000 mouse developmental cDNA microarray, 2000,
 Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
 Large-scale cDNA analysis reveals phased gene expression
 patterns during preimplantation mouse development, 2000,
 Development, 128: 553-561; (3) Gene expression of
 unselected transcripts from extraembryonic tissue of
 7.5 day mouse embryos reveals contribution to the complex
 and under representation on the X chromosome, 1998, Hum
 Mol Genet 7: 1967-1978.
 MGI Genet 7: 1967-1978.
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US-09-479-862-1 x AAV-95463

Align seq 123 x AAV-95463 Size 1 x 1000

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1 TyrPheGlyLysIleuSerLysAspSerValIleValAsnIleuAsnAs 17
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543 TACTTGGCAAGCTGCAATTAAGATATAGAGTAAAGAAATTTGAGTAA 542
17 pGluValLeuPheIleAspGlnGlyAsnAlaGlnProLeuPheGluAspMet 44
|||||
594 CCAAGTCTCTTCACTGAGCAAGCAAAATGAGATCTATTTCAGAAATAGA 642
24 LeuAspGlnAspGlnSerValIleValAsnIleuSerValIleValAsn 60
|||||
643 CTGATCTGACGTGATAGATAAAGATAGCAAGCAAGCAATATTATTAAGT 692
51 MetTyrLysAspSerValProGlyIleuSerValIleValAsnIleuSer 67
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693 ATGATATAAGATAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 742
67 scysGlnLysIleuSerValIleValAsnIleuSerValIleuSerPheL 84
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743 GGTGAGAGAAATTTCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 792
84 ysgIleuMetAspProLeuAspAsnIleuLysAspIleuLysSerAspIleu 100
|||||
793 AGCAAAATGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 842
101 PhePheGlnArgSerValProGlyIleuSerValIleValAspAsnMetGln 117
|||||
843 TTCCTTCAGAGCAAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 892
117 rSerSerTyrGlnIleuSerValIleValAsnIleuSerValIleuSerP 134
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893 TTGATCAATAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 942
134 heLysIleuIleuLysGlnAspIleuLysAspIleuLysSerIleuMet 150
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943 TTAAATCAATTTTCAAAAAAGAGATGCAATTTGAGCAATAGATATAAG 992
151 PheIleValGlnAsnGluAsp 157
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993 TTCACCTGTTCAAAACCAAGSAC 1013

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seq_name: 237533 chr1:100000000-100000000, hg19 chr1:100000000-100000000

seq_documentation_block:

id: AAT32411; standard: cDNA to mRNA, 471 bp.

XX AAT32411;

XX 29-SEP-1996 (first entry)

XX Human interferon gamma inducer protein cDNA.

XX Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;

KW anti-tumour; anti-bacterial; immunoregulatory; adoptive immunotherapy;

KW therapy; cancer; ds.

XX Homo sapiens.

XX EF712931-A2.

XX 22-MAY-1996.

XX 10-NOV-1995; 95JP-0408055

XX 29-SEP-1995; 95JP-0274988.

XX 15-NOV-1994; 94JP-0404203.

XX 24-FEB-1995; 95JP-0058240.

XX 10-MAR-1995; 95JP-0078357.

XX 18-SEP-1995; 95JP-0262062.

id: us-09-479-862-1; standard: AAV-95463.

XX 13-DEC-1996; Fujita T., Fujita T., M., Tamura H.

XX Taniguchi M., Tanimoto T., Toriabe K., Ushio S.

XX WPI; 1996-252837/26.

XX E-mail: AAV95463.

XX DNA encoding interferon gamma protein, inducing polypeptide, used for

XX to treat and prevent, e.g., viral disease, malignancies and immune

XX disorders

XX E-mail: 95463, E-mail: 28; 48pp; English.

XX A cDNA clone (AAT32411) codes for a novel human protein (AAV95463) that

XX induces interferon gamma (IFN gamma) protein by immunocompetent cells.

XX It was isolated as a plaque DNA clone from a human liver library.

XX PCR amplification of the sequence (see also AAT32409-10) and expression

XX in Escherichia coli XL-1 Blue MRF'kan allowed production of recombinant

XX inducer protein. This was used to construct hybridoma H 1-3 which

XX produced anti-IFN gamma inducer protein monoclonal antibody H 1A8.

XX useful in the detection and purification of the inducer protein (see

XX also AAV95554).

XX Sequence 471 bp; 166 A; 76 C; 88 G; 140 T; 1 other;

alignment_score:

quality: 810.00 Length: 157

Ratio: 5.192 Gaps: 0

Percent similarity: 99.463 Percent identity: 99.463

alignment_block:

US 09-479-862-1 x AAT32411

Align seq 1/1 to: AAT32411 from: 1 to: 471

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1 TACTTGGCAAGCTGCAATTAAGATATAGAGTAAAGAAATTTGAGTAA 50

17 pGluValLeuPheIleAspGlnGlyAsnAlaGlnProLeuPheGluAspMet 34

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51 CCAAGTCTCTTCACTGAGCAAGCAAAATGAGATCTATTTCAGAAATAGA 100

34 hrAspSerAspGlnAspAsnAlaGlnProLeuPheIleuSer 50

|||||

161 CTGATCTGACGTGATAGATAAAGATAGCAAGCAAGCAATATTATTAAGT 150

51 MetTyrLysAspSerGlnProLeuPheIleValIleuSerValIle 67

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151 ATGATATAAGATAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 200

67 scysGlnLysIleuSerValIleValAsnIleuSerValIleuSerPheL 84

|||||

201 GTGTGAGAGAAATTTCAACTCTCTCTCTCTCTCTCTCTCTCTCTCT 250

94 scysGlnLysIleuSerValIleValAsnIleuSerValIleuSerPheL 100

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251 AGGAAATGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300

101 PhePheGlnArgSerValProGlyIleuSerValIleValAspAsnMetGln 117

|||||

401 TTCTTTCAGAGCAAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 450

117 rSerSerTyrGlnIleuSerValIleValAsnIleuSerValIleuSerP 134

|||||

451 TTGATCAATAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 480

134 heLysIleuIleuLysGlnAspIleuLysAspIleuLysSerIleuMet 150

|||||

401 TTAAATCAATTTTCAAAAAAGAGATGCAATTTGAGCAATAGATATAAG 450

XX A drug containing a polypeptide which induces interferon gamma
 PI useful for treating e.g. malignant tumours, viral, bacterial or
 PI immune diseases
 XX Disclosure: Page 9-10; 12pp; Japanese.
 XX This sequence encodes a protein which induces interferon gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 XX
 XX Sequence 471 BP; 166 A; 76 C; 88 G; 140 T; 1 other;

alignment_scores:
 Quality: 810.00 Length: 157
 Ratio: 5.192 Gaps: 0
 Percent Similarity: 99.363 Percent Identity: 99.363

alignment_block:

US-09-479-862-1 x AAZ46875

Align seq 1/1 to: AA180209 from: 1 to: 471

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1 TyrPheGlyIleGluGlnSerIleGluSerValThrArgAsnLeuAspAs 17
1 TACTTGGCAAGCTTGAATCTAAATATACAGGATTAAGAAATTTCTGAAGA 50
17 PheValIleGluPheGlnAspGlnGlyAsnArgProGluPheGlnAspMet 34
51 GCAAGTTCCTCTATTGACGACAAAGAAATCGAGTCTATTTGAGGATATGA 100
34 ArgAspSerAspGlyAsnArgAsnAsnAlaArgArgArgGlnPheGlnHis 56
101 GTCATCTGACCTGTACAGATTAATGCAATCCGAGACGACATATATTATTA 150
51 MetIleValAspSerGluProArgGlyMetAlaValThrIleSerValThr 67
151 ATGATATAAAGATAGTACAGGCTTAAGAGGATAGTGTGAGGATATCTGTGA 200
67 SCysAlaValThrSer***LeuSerGlySerGlnAsnGlyThrIleSerPhe 84
201 GTGTGCAAAATTTCAATTTCTCTGTGAGACAAAGAAATTAATTTCTTTA 250
84 ValGluMetAsnProArgAspAsnAlaValAspPheValIleThr 100
251 AGCAATGCAACCTTCCCTATAAATATGAAGATACAAAGAAATGATATATA 300
101 PhePheGlnArgSerValProGlyHisAspAsnGlyMetGlnPheHisLac 117
401 TTCCTTCAGACAAAGTGTCAGAGACACAGACAGACAGATTAATGATGAAAT 350
117 rSerSerTyrGlnGlyTyrPheGluAlaCysGlnGlySerGlnArgAspMet 134
451 TTCATATATACAGAGATATTTCTAGTTCGTAAAAAAATGAGAGAGATTT 400
134 PheValIleuIleLeuIleValGlySerGlnAspGlnLeuGlyAspArgSer 150
401 TTAAGATTAATTTTGAAGAAAGACATGATTTGAGGATATGATATGATAG 450
151 PheThrValGlnAsnLeuAsp 157
451 TTCATTCGATGAAAAAGAAAGAC 471

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seq.name: US-09-479-862-1 p2n.rng file name: US-09-479-862-1

seq.documentalation_block:

10 AAZ46875 standard. DNA. 471 bp.

XX

AC AAZ46875;

XX

14 13 MAK zmm (first entry)
 XX
 XX DNA encoding a mature protein that induces IFN-gamma production
 XX
 KW Human: interferon gamma production; IFN-gamma; immunocompetent cells
 KW antiviral; immunoregulatory; antileukemia; antitumor;
 KW IFN-gamma susceptible disease; antibacterial; antitumor;
 KW blood platelet enhancing agent; hepatitis; herpes syndrome; candida
 KW AIDS; bacterial disease; candidiasis; malaria; solid malignant tumor;
 KW renal cancer; mycosis; tumours; chronic granulomatous disease;
 KW blood cell malignant tumor; adult T cell leukaemia;
 KW chronic myelogenous leukaemia; malignant leukaemia; immune diseases;
 KW allergy; rheumatism; ss.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FE CDS 1..471
 FI /*tag a
 FI Accession: US-09-479-862-1 p2n.rng
 FI Note: "Xaa is Ile or Thr"
 XX
 XX EF562541 Aa.
 XX
 XX 08 DEC 1999.
 XX
 XX 10 NOV 1995; 99EP-0104104.
 XX
 XX 15 NOV 1994; 94JP-0004204.
 PR 23 FEB 1995; 95JP-0098240.
 PR 10 MAR 1995; 95JP-0078357.
 PR 18 SEP 1995; 95JP-0242062.
 PR 29 SEP 1995; 95JP-0274988.
 PR 10 NOV 1995; 95EP-0308055.
 XX
 XX (BAYB) HAYASHIBARA SEIICHI KAGAKU.
 XX
 XX Toshio S. Toriue K. Tanimoto I. Okamura H;
 XX
 XX WPI: 2000 064289/06.
 PR
 PR FTSU: AA55904.
 XX
 XX Novel polypeptides used in the treatment of interferon-gamma
 susceptible diseases
 PS
 PS Claim 9; Page 6; 42pp; English.
 XX
 XX The present sequence encodes a human protein that induces interferon
 CC gamma production by immunocompetent cells. IFN-gamma is a
 CC protein which has antiviral, antitumor and immunoregulatory activities,
 CC and is produced by immunocompetent cells stimulated with antigens or
 CC mitogens. The protein of the invention is used to treat IFN-gamma
 CC susceptible diseases, and also have use as an antiviral agent,
 CC antibacterial agent, antitumor agent, immunoregulatory agent and blood
 CC platelet enhancing agent. Diseases which can be treated with the
 CC protein include viral diseases such as hepatitis, herpes syndrome,
 CC candida, and AIDS; bacterial diseases such as candidiasis and
 CC malaria; solid malignant tumours such as renal cancer, mycosis
 CC tumours, and chronic granulomatous disease; blood cell malignant
 CC tumours such as adult T cell leukaemia, chronic myelogenous leukaemia
 CC and malignant leukaemia; and immune diseases such as allergy and
 CC rheumatism.
 XX
 XX Sequence 471 BP; 166 A; 76 C; 88 G; 140 T; 1 other;

alignment_scores:

Quality: 810.00 Length: 157

Ratio: 5.192 Gaps: 0

Percent Similarity: 99.363 Percent Identity: 99.363

alignment_block:

US-09-479-862-1 x AAZ46875

genome version 4.5
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96 nucleic nucleic search using sw model

Run on: August 2, 2001, 04:58:13 : Search time: 00:09.11 seconds
(without alignments)
664,500 Million cell updates/sec

Title: us-09-479-862-3
Portect score: 135
Sequence: 1 GAAAGCTGGAGACAGATTAC.....GAGAGATTCAGAGAGAG 135

Sorted Table: IDENTITY_NUC
Gapop 10.0 : Gapext 1.0
Searched: 1344157 seqs, 774874588 residues
Total number of hits satisfying chosen parameters: 2600414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: qb_ba2 : *

3: qb_ba3 : *

4: qb_ba4 : *

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93: qb_ba93 : *

94: qb_ba94 : *

95: qb_ba95 : *

96: qb_ba96 : *

97: qb_ba97 : *

98: qb_ba98 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being pointed out, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	135	100.0	135	E15642	E15642: Homo sapiens
2	135	100.0	136	HS295724	HS295724: Homo sapiens
3	135	100.0	579	AR069452	AR069452: Streptococcus
4	135	100.0	579	E15603	E15603: Homo sapiens
5	135	100.0	579	HS090434	HS090434: Homo sapiens
6	135	100.0	1102	D49950	D49950: Homo sapiens
7	135	100.0	1120	E14759	E14759: Homo sapiens
8	135	100.0	1120	E15641	E15641: Homo sapiens

[illegible]

52805 68147 cont'd of 15433 bp in length
68238 79859 cont'd of 15602 bp in length
79940 90772 cont'd of 16833 bp in length
90873 103693 cont'd of 12821 bp in length
103704 113479 cont'd of 10124 bp in length
114018 122609 cont'd of 8592 bp in length
122710 129672 cont'd of 6863 bp in length
129673 135802 cont'd of 6160 bp in length
135903 140049 cont'd of 4147 bp in length
140150 144259 cont'd of 4110 bp in length
144360 148078 cont'd of 3719 bp in length
148179 152182 cont'd of 4004 bp in length
152283 156213 cont'd of 2941 bp in length
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M nucleotide - nucleotide search, using SW model

Run on: August 2, 2001, 04:55:58 : Search time: 206.44 seconds
(without alignments)
335,964 million cell updates/sec

Title: US-09-479-862-3
Perfect score: 135
Sequence: 1 AAAAATGGAAATCAATTAAT.....GATGCAATGACTCTATAG 145

Scoring table: IDENTITY_NW
Gapop 10.0 / Gapext 1.0

Searched: 1028115 seqs, 4726426760 testbases
Total number of hits satisfying chosen parameters: 20456240

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0K
Maximum Match 100K
Listing first 45 summaries

Database:

EST:

1: qb_est1: *
2: qb_est2: *
3: qb_est3: *
4: qb_est4: *
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61: qb_est61: *
62: qb_est62: *
63: qb_est63: *
64: qb_est64: *
65: qb_est65: *
66: qb_est66: *
67: qb_est67: *
68: qb_est68: *
69: qb_est69: *
70: qb_est70: *
71: qb_est71: *
72: qb_est72: *
73: qb_est73: *
74: qb_est74: *
75: qb_est75: *
76: qb_est76: *
77: qb_est77: *
78: qb_est78: *
79: qb_est79: *
80: qb_est80: *
81: qb_est81: *
82: qb_est82: *
83: qb_est83: *
84: qb_est84: *
85: qb_est85: *
86: qb_est86: *
87: qb_est87: *
88: qb_est88: *
89: qb_est89: *
90: qb_est90: *
91: qb_est91: *
92: qb_est92: *
93: qb_est93: *
94: qb_est94: *
95: qb_est95: *
96: qb_est96: *
97: qb_est97: *
98: qb_est98: *
99: qb_est99: *
100: qb_est100: *
101: qb_est101: *
102: qb_est102: *
103: qb_est103: *
104: qb_est104: *
105: qb_est105: *
106: qb_est106: *
107: qb_est107: *
108: qb_est108: *
109: qb_est109: *
110: qb_est110: *
111: qb_est111: *
112: qb_est112: *
113: qb_est113: *
114: qb_est114: *
115: qb_est115: *
116: qb_est116: *

XX
 PN BP712931-AZ.
 XX
 PD 22-MAY-1996.
 XX
 PF 10-NOV-1995; 95JP-0308055.
 XX
 PR 29-SEP-1995; 95JP-0274998.
 PK 15-MAY-1994; 94JP-0304283.
 PR 27-FEB-1993; 93JP-0052240.
 PR 10-MAR-1995; 95JP-0078357.
 PR 18-SEP-1995; 95JP-0262062.
 XX
 PA (HAYB) HAYASHIBARA SEIICHIRO KAGAKU.
 XX
 PI Fukuda S, Kohae K, Kurikata I, Torioka K, Okamura M,
 PI Taniguchi M, Tanimoto T, Torioka K, Oshio S;
 XX
 PR WPI: 1996-252837/26
 PR P PSDB: AAK69566.
 XX
 PI DNA encoding interferon gamma produ. inducing polypeptide, useful
 PI to treat and prevent, e.g. viral disease, malignancies and immune
 PI disorders
 XX
 PS claim 6; Page 41-42; 48pp; English.
 XX
 CC A full-length cDNA clone (AAT42404) codes for a novel human protein
 CC (AAK69560), the mature portion of which (see also AAK69568) induces
 CC interferon-gamma (IFN-gamma) produ. by immunocompetent cells. The
 CC clone was cloned from a human liver cDNA library in pSeri-His
 CC and by screening with a probe based on a murine IFN-gamma inducer
 CC protein cDNA (see also AAT42401). The cDNA, or the portion of it
 CC (AAT42402) coding for the mature protein, can be used for the high yield
 CC produ. of IFN-gamma inducer protein, esp. in transformed E. coli host
 CC cells. The protein is useful as an antiviral, antitumor,
 CC antibacterial, immunoregulatory and blood platelet enhancing agent.
 XX
 SQ Sequence 1120 bp; 379 A; 227 C; 231 G; 283 T; 1 other;

Query Match 100.0%; Score 145; DB 17; Length 1120;
 Best local similarity: 100.0%; Pred. No. 76 32;
 Matches 145; Conservative 0; Mismatches 0; Gaps 0;
 QY 1 AAAAACTGGAAATCAGATTACTTTTGGTAAAGTTGAATCTTAAATATATCAATATATAAAAT 60
 DB 269 aaacctgaatcaatcaattacttttgaacattgaattcaattcaattcaattcaattcaatt 328
 QY 61 TGAATGAGCAAGTCTCTCTTCATATGACCAAGGAAATGGGCTCTATTGGAATATATAT 120
 DB 329 tgaataaacaattctcttcaattgaacaaagaatcgaactctattgaatatatcaatt 388
 QY 121 ATTTCGATGAGAG 135
 DB 389 atttcaattatadaa 404

RESULT 4
 AAV15825
 ID AAV15825 standard; cDNA to mRNA; 1120 bp.
 AC AAV15825;
 DT 05-JUN-1998 (first entry)
 XX cDNA for interferon-gamma production inducer.
 DE
 XX Interferon-gamma; IFN gamma; production inducer; gene therapy;
 KW immunocompetent cell; treatment; prevention; malignant tumors;
 KW viral infection; bacterial infection; immune disease; ds.
 XX Homo sapiens.
 OS

XX
 FH Key location/qualifiers
 FT CDS 178..759
 FT /*taad 178..285
 FT s14_pept_ida 178..285
 FT /*taad 286..756
 FT mat_pept_ida 286..756
 FT /*taad 286..756
 FT Zoned_peptide (pos.582..584, aa.Xaa)
 FT Note "Xaa unknown"
 PN EP816499 A2.
 XX
 PD 07 JAN 1998.
 XX
 DT 27-JAN-1997; 97EP-0304516.
 XX
 PR 27-JUN-1996; 96JP-0185405.
 XX
 PA (HAYB) HAYASHIBARA SEIICHIRO KAGAKU.
 XX
 PI Kurimoto M, Okura T, Torioka K;
 XX
 PR WPI: 1998-054914/06.
 PR P PSDB: AAM47429.
 XX
 PI Genomic DNA encoding polypeptide inducing interferon-gamma
 PI production - by immuno-competent cells, useful to treat e.g. human
 PI malignant tumors or viral diseases
 XX
 PS claim 2; Pages 49-50; 74pp; English.
 XX
 CC The present sequence encodes a protein, which induces
 CC interferon gamma (IFN gamma) production in immunocompetent cells.
 CC The protein has high biological activity, including enhancing
 CC cytotoxicity of killer cells and inducing killer cell formation.
 CC In addition to inducing IFN-gamma production by immunocompetent
 CC cells when expressed in mammalian cells, facilitating its use in
 CC low dosage to treat/prevent e.g. malignant tumors, viral or
 CC bacterial infections and immune diseases. As it is expressed in
 CC mammalian cells, it also has low toxicity when used in human
 CC treatments, minimising side effects. The DNA encoding the protein
 CC can be used in gene therapy, e.g. by infecting vectors containing
 CC the DNA or transplanting cells.
 XX
 SQ Sequence 1120 bp; 379 A; 227 C; 231 G; 283 T; 1 other;

Query Match 100.0%; Score 145; DB 19; Length 1120;
 Best local similarity: 100.0%; Pred. No. 76 32;
 Matches 145; Conservative 0; Mismatches 0; Gaps 0;
 QY 1 AAAAACTGGAAATCAGATTACTTTTGGTAAAGTTGAATCTTAAATATATCAATATATAAAAT 60
 DB 269 aaacctgaatcaatcaattacttttgaacattgaattcaattcaattcaattcaattcaatt 328
 QY 61 TGAATGAGCAAGTCTCTCTTCATATGACCAAGGAAATGGGCTCTATTGGAATATATAT 120
 DB 329 tgaataaacaattctcttcaattgaacaaagaatcgaactctattgaatatatcaatt 388
 QY 121 ATTTCGATGAGAG 135
 DB 389 atttcaattatadaa 404

RESULT 5
 AAZ36876
 ID AAZ36876 standard; cDNA to mRNA; 1120 bp.
 XX
 AC AAZ36876;
 XX
 DT 14-MAR-2000 (first entry)
 XX

GeneCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

CM nucleic = nucleic search, using sw model

Run on: August 2, 2001, 07:12:24 : Search time 0'99.11 Seconds
(without alignments)
9061.264 Million cell updates/sec

Title: US-09-479-862 7
Perfect score: 2167
Sequence: 1 GAAATGAAATGATGATGAA.....AGGATGAAATGATGATGAT 2167

Scoring table: IDENTITY_ND*
Gapop 10.0 : Gapext 1.0

Searched: 144457 seqs, 773467466 residues 2688414
Total number of hits satisfying chosen parameters:

Minimum db seq length: 6
Maximum db seq length: 20000000

Post-processing: Minimum Match OK
Maximum Match 100%
Fastest First 45 summaries

Database:

GenEntrez:
1: ab_ba1:
2: ab_ba2:
3: ab_ba3:
4: ab_ba4:
5: ab_ba5:
6: ab_ba6:
7: ab_ba7:
8: ab_ba8:
9: ab_ba9:
10: ab_ba10:
11: ab_ba11:
12: ab_ba12:
13: ab_ba13:
14: ab_ba14:
15: ab_ba15:
16: ab_ba16:
17: ab_ba17:
18: ab_ba18:
19: ab_ba19:
20: ab_ba20:
21: ab_ba21:
22: ab_ba22:
23: ab_ba23:
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26: ab_ba26:
27: ab_ba27:
28: ab_ba28:
29: ab_ba29:
30: ab_ba30:
31: ab_ba31:
32: ab_ba32:
33: ab_ba33:
34: ab_ba34:
35: ab_ba35:
36: ab_ba36:
37: ab_ba37:
38: ab_ba38:
39: ab_ba39:
40: ab_ba40:
41: ab_ba41:
42: ab_ba42:
43: ab_ba43:

44: cm_ov:
45: cm_pat:
46: cm_ph:
47: cm_pl:
48: cm_to:
49: cm_sts:
50: cm_sy:
51: cm_uo:
52: cm_vl:
53: qb_sts1:
54: qb_sts2:
55: qb_sts3:
56: qb_sy:
57: qb_uo:
58: qb_vl:
59: qb_vl2:
60: qb_btq1:
61: qb_btq2:
62: qb_btq3:
63: qb_btq4:
64: qb_btq5:
65: qb_btq6:
66: qb_btq7:
67: qb_btq8:
68: qb_btq9:
69: qb_btq10:
70: qb_btq11:
71: qb_btq12:
72: qb_btq13:
73: qb_btq14:
74: qb_btq15:
75: qb_btq16:
76: qb_btq17:
77: qb_btq18:
78: qb_btq19:
79: qb_btq20:
80: qb_btq21:
81: qb_btq22:
82: qb_btq23:
83: qb_btq24:
84: qb_btq25:
85: qb_pr1:
86: qb_pr2:
87: qb_pr3:
88: qb_pr4:
89: qb_pr5:
90: qb_pr6:
91: qb_pr7:
92: qb_pr8:
93: qb_pr9:
94: qb_r01:
95: qb_r02:
96: qb_r04:
97: qb_pr10:
98: cm_ba3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	2167	100.0	2167	10	E15646
2	2167	100.0	28994	10	E15653
3	2150.2	99.2	161920	83	AF002502
4	2149.2	99.2	187516	61	AF009648
5	2145.4	99.0	167069	73	AF006783
6	2145.4	99.0	168922	91	AF002007
7	2145.4	99.0	172859	61	AF010815
8	562.2	25.9	1120	10	E14759

[illegible]

[illegible]


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Query Match      100.0%; Score 134; 1b 21; Length 551;
Best Local Similarity 100.0%; Pred. No. 76-83;
Matches 134; Conservative 0; Mismatches 0; Gaps 0;

QY 1 ATAAAGACCGAGACATATATATTAAGTATGTAAGAGATAGGAGAGAGTAAAGGTA 60
1b 1aataaqeececeqaacatattatataatataatataatataatataatataatata 250
QY 61 TGGTGTGAATATCTGTGTGAAGTGTGAAGAAATTTCAATGCTGTGTGTGTGTGAAGAA 120
1b 1aataatataatataatataatataatataatataatataatataatataatataat 310
QY 121 TATTTCTTTTAAAG 134
1b 1aataatataatataatataatataatataatataatataatataatataatataat 320

RESULT 4
AAV42754
1b AAV42754 standard: cDNA; 570 bp.
XX AC
XX AAV42754:
XX 25-SEP-1998 (first entry)
XX
XX Wild-type human interferon-gamma inducing factor cDNA.
XX
XX Interferon gamma induced factor; Interferon-gamma; killer cell;
XX antitumor agent; antiviral agent; antimicrobial agent; Tumor; IGIF;
XX hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
XX osteoporosis; thrombopenia; acquired immunodeficiency syndrome; ds.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX 5'UTR 1-15
XX /star a
XX CDS 16-558
XX /star b
XX /product "Immature human IGIF"
XX 16-184
XX /star c
XX /note "this sequence obtained by the invention"
XX
XX mat_peptide 85-558
XX /star d
XX CUIR 559-570
XX /star e
XX
XX EP845540 A2.
XX
XX 6-6-JUN-1998.
XX
XX 28-NOV-1997; 97EP-0309632.
XX
XX 14-NOV-1997; 97JP-0329715.
XX 29-NOV-1996; 96JP-0343047.
XX 21-JAN-1997; 97JP-0020506.
XX
XX (HAYE ) HAYASHIHARA SEIICHIRO KAWAKO
XX Kurumatsu M. et al. Nature 371, 446-449;
XX
XX WP1: 1998-282747/26
XX P-FSD8: AAW48959.
XX
XX Mutants of interferon-gamma inducing polypeptide useful as
XX antitumor, antiviral, antimicrobial or anti-immunophagic agents
XX
XX claim 11: pages 36-37; 59pp; English
XX

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The present sequence represents the wild-type human interferon-gamma
inducing factor (IGIF) cDNA. The invention provides for mutant human
and mouse interferon-gamma inducing factors in which one or more
cysteine residues are replaced with different residues at 67 and 76. In
the consensus sequences shown in AAW48959, W48958. The mutant IGIFs are
capable of stimulating immunocompetent cells for the production of
interferon-gamma and are claimed to be less toxic, more active and
stable than the corresponding wild type interferon-gamma inducing
factor. The mutant IGIFs are also claimed to enhance killer cell
cytotoxicity and/or induce killer cell formation, and may therefore
be useful as antitumor agents, antitumor immunotherapeutics, and/or as
agents and/or microbial agents. The mutant IGIFs are also claimed
to be useful for treating hepatitis, acquired immunodeficiency syndrome
(AIDS), malaria, tuberculosis, solid malignant tumors (e.g., renal
carcinoma), rheumatism, osteoporosis and thrombopenia caused by
radiation- and chemo-therapy.
XX Sequence 570 bp; 179 A; 109 C; 117 G; 165 T; 0 other.
SQ

Query Match      100.0%; Score 134; 1b 19; Length 576;
Best Local Similarity 100.0%; Pred. No. 7,10-33;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1
1b 1aataatataatataatataatataatataatataatataatataatataatataat 200
QY 61 TGGTGTGAATATCTGTGTGAAGTGTGAAGAAATTTCAATGCTGTGTGTGTGTGAAGAA 120
1b 1aataatataatataatataatataatataatataatataatataatataatataat 260
QY 121 TATTTCTTTTAAAG 134
1b 1aataatataatataatataatataatataatataatataatataatataatataat 320

RESULT 5
AAV62200
1b AAV62200 standard: DNA; 582 bp.
XX AC
XX AAV62200:
XX 6-DEC-2001 (first entry)
XX
XX cDNA encoding a human IL-18 with a caspase 3 cleavage site.
XX
XX Induced cleavage site; Caspase 3; Interleukin-18; IL-18; proteinase 3;
XX Synthesized.
XX Homo sapiens.
XX
XX WP2000061768 A2.
XX
XX 19-NOV-2000.
XX
XX 14-APR-2000; 2000WO-1140220.
XX
XX 14 APR 1999; 99JP-0129427.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Robinson M. Liu R. Novick D. Binarello G. Graber F.
XX
XX WP1: 2001-066910/01.
XX P-FSD8: AAW40641.
XX
XX Preparation of biologically active molecules from its inactive
XX precursors, comprises mutating their native cleavage site to a site
XX capable of being cleaved by protease and cleaving the mutated molecule
XX
XX Disclosure: Fig 8a-b; 40pp; English.
XX

```


[illegible]

us-09-479-862-4.rng

Thu Aug 2 10:26:52 2001

GenCore version 4.5
Copyright (c) 1992-2000 Compaq Inc.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2001, 06:07:55 : Search time 4798.42 seconds
(without alignments)
333.475 Million cell updates/sec

Title: 08-09-479-862-4

Perfect score: 134

Sequence: 1 ATAATGACACCCAGACATA.....ACAAATTAATTCCTTTAAG 134

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 10228115 seqs, 472642650 residues

Total number of hits satisfying chosen parameters: 20456210

Minimum OR seq length: 0

Maximum OR seq length: 2000000000

Post-processing: Minimum Match: 9%

Maximum Match: 100%

Listing first 45 summaries

Database:

EST:

1: qb_est1: *
2: qb_est2: *
3: qb_est3: *
4: qb_est4: *
5: qb_est5: *
6: qb_est6: *
7: qb_est7: *
8: qb_est8: *
9: qb_est9: *
10: qb_est10: *
11: qb_est11: *
12: qb_est12: *
13: qb_est13: *
14: qb_est14: *
15: qb_est15: *
16: qb_est16: *
17: qb_est17: *
18: qb_est18: *
19: qb_est19: *
20: qb_est20: *
21: qb_est21: *
22: qb_est22: *
23: qb_est23: *
24: qb_est24: *
25: qb_est31: *
26: qb_est34: *
27: qb_est35: *
28: qb_est36: *
29: qb_est37: *
30: qb_est38: *
31: qb_est39: *
32: qb_est40: *
33: em_estba: *
34: em_estfun: *
35: em_esthum1: *
36: em_esthum2: *
37: em_esthum3: *
38: em_esthum4: *
39: em_esthum5: *
40: em_esthum6: *
41: em_esthum7: *
42: em_esthum8: *
43: em_esthum9: *

44: em_esthum10: *
45: em_esthum11: *
46: em_esthum12: *
47: em_esthum13: *
48: em_esthum14: *
49: em_esthum15: *
50: em_esthum16: *
51: em_esthum17: *
52: em_esthum18: *
53: em_esthum19: *
54: em_esthum20: *
55: em_esthum21: *
56: em_esthum22: *
57: em_esthum23: *
58: em_esthum24: *
59: em_esthum25: *
60: em_esthum26: *
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66: em_estin4: *
67: em_estin5: *
68: em_estin1: *
69: em_estin2: *
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71: em_estov2: *
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75: em_estp14: *
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77: em_estp16: *
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92: em_estrol11: *
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105: qb_est28: *
106: qb_est29: *
107: qb_est30: *
108: qb_est31: *
109: qb_est32: *
110: qb_est41: *
111: qb_est42: *
112: qb_est43: *
113: qb_est44: *
114: qb_est45: *
115: qb_est46: *
116: qb_est47: *

```

117: qb_est10: *
118: qb_est11: *
119: qb_est12: *
120: qb_est13: *
121: qb_est14: *
122: qb_est15: *
123: qb_est16: *
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125: qb_est18: *
126: qb_est19: *
127: qb_est20: *
128: qb_est21: *
129: qb_est22: *
130: qb_est23: *
131: qb_est24: *
132: qb_est25: *
133: qb_est26: *
134: qb_est27: *
135: qb_est28: *
136: qb_est29: *
137: qb_est30: *
138: qb_est31: *
139: qb_est32: *
140: qb_est33: *
141: qb_est34: *
142: qb_est35: *
143: qb_est36: *
144: qb_est37: *
145: qb_est38: *
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147: qb_est40: *
148: qb_est41: *
149: qb_est42: *
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152: qb_est45: *
153: qb_est46: *
154: qb_est47: *
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158: qb_est51: *
159: qb_est52: *
160: qb_est53: *
161: qb_est54: *
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163: qb_est56: *
164: qb_est57: *
165: qb_est58: *
166: qb_est59: *
167: qb_est60: *
168: qb_est61: *
169: qb_est62: *
170: qb_est63: *
171: qb_est64: *
172: qb_est65: *
173: qb_est66: *
174: qb_est67: *
175: qb_est68: *
176: qb_est69: *
177: qb_est70: *
178: qb_est71: *
179: qb_est72: *
180: qb_est73: *
181: qb_est74: *
182: qb_est75: *
183: qb_est76: *
184: qb_est77: *
185: qb_est78: *
186: qb_est79: *
187: qb_est80: *
188: qb_est81: *
189: qb_est82: *

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID
1	134	100.0	655	227	AQ377384
2	134	100.0	684	32	AV733501
3	134	100.0	752	131	BF768246
4	134	100.0	756	113	AF555675
5	122	91.0	861	145	BF267619
6	112	83.6	888	154	AF556861
7	110.2	82.2	763	124	AF550065
8	110	81.1	634	31	AF556841
9	106.8	79.7	443	31	AV597984
10	106.8	79.7	574	31	AV597985
11	101	75.4	374	139	BF715167
12	97.2	72.5	782	137	BF565347
13	83.4	62.2	497	151	BF652935
14	81	60.4	834	156	BF212957
15	76	56.7	564	149	BF455617
16	76	56.7	512	111	AF125192
17	76	56.7	564	173	BC088927
18	76	56.7	603	13	AA930362
19	76	56.7	713	142	BF979995
20	75.1	56.2	672	137	BF565892
21	74.4	55.5	499	173	BC076382
22	71.4	55.5	646	13	AA92285
23	65.4	48.8	474	16	AF121820
24	63.2	47.2	460	151	BF668764
25	63.2	47.2	434	4	AA237736
26	42.8	21.5	423	177	AF558749
27	37.2	27.8	163	235	AF151342
28	36	26.9	129	120	AF830713
29	35.6	26.6	289	4	AA245593
30	35.4	27.4	163	20	AF145001
31	32.6	24.3	835	146	BF218980
32	31.8	23.7	641	276	BF3648
33	31.8	23.7	941	220	CNS02431
34	31.6	23.6	354	145	BF168847
35	31.6	23.6	423	3	AF162729
36	31.6	23.6	135	3	AA244433
37	31.6	23.6	435	12	AA823217
38	31.6	23.6	425	115	AF411949
39	31.6	23.6	458	167	BF448506
40	31.6	23.6	465	2	AA204187
41	31.6	23.6	491	11	AA759760
42	31.6	23.6	500	139	BF693027
43	31.6	23.6	524	136	BF532679
44	31.6	23.6	538	136	BF532675
45	31.6	23.6	564	4	AA277295

ALIGNMENTS

RESULT	1
AQ377384	AQ377384 655 bp TNA
DEFINITION	RPCL11-163A13.1J RPCL11 Homo sapiens genomic clone RPCL11 163A13, DNA sequence.
ACCESSION	AQ377384
VERSION	AQ377384.1 GI:4348407
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	Zhao, S., Adams, M.D., Niernan, W., Malek, J., de Jong, P., and Venter, J.C.
TITLE	Use of HAC End Sequences from Library RPCL11 for Sequence Ready Map Building

JOURNAL COMMENT

Unpublished (1997)
 Contact: Shaying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeet@tigr.org
 Clones are derived from the human BAC library RPCL11. For BAC library availability, please contact Peter de Jong (peter@tigr.org, med.bal@tigr.org). Clones may be purchased from "BAC" Resources (http://bacpac.med.bal@tigr.org/order) or from Research Genetics (http://genetec.com). BAC end search paper: http://www.tigr.org/ftp/ftp.hmp.org/bac_end_search.html
 Seq primer: SP6
 Class: HAC ends.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="Gen:756220"
 /db_xref="taxon:9606"
 /clone="RPCL11-163A13"
 /accession="RPCL11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: PRACE3.6; Site:1: EcoRI; Site 2: EcoRI; RPCL11 Human Male BAC Library"
 BASE COUNT 229 a 104 c 93 g 0 t
 ORIGIN

Query Match 100.0% Score 194; DB 227; Length 655;
 Real-Score Similarity: 100.0%; Prod. Ratio: 29;
 Matches 134; Mismatch: 0; Re-matches 0; Indels 0; G4 0;
 57 1 A T A A G C A A C C G A C A A T A T A T A T A A G A G A G A T A A A G A T A C C A G A C A G A G A A 60
 134 38 A T A A T C A A C C G A C A A T A T A T A T A A G A G A G A T A A A G A T A C C A G A C A G A 97
 207 61 T G C T C T A T A T A T C T C T G T A A C T C A A G A A A T T T A A C T C T C T C T C T C A C A N A A A 120
 146 93 G A G C G C A A G A T A G C A G A A G C A C A G A A A A T T A A C T C T C T C T C T C T C A G A A A A 157
 207 121 T T A T T C C T T T A A G 134
 146 158 T T A T T C C T T T A A G 171

FEATURES

DEFINITION AV733501 684 bp mRNA
 ACCESSION AV733501
 VERSION AV733501.1 GI:10851046
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

Adinolfi
 1 (bases 1 to 684)
 Zhao, S., de Jong, P., Adams, M.D., Niernan, W., Malek, J., de Jong, P., and Venter, J.C.
 201203, P. R. China
 Tel: 86 21 50801919 (ex.45)
 Fax: 86 21 50801922
 Email: hanzq@tigr.sh.cn

TITLE

Homo sapiens cDNA clones
 Unpublished (2000)
 Contact: Zengqiang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86 21 50801919 (ex.45)
 Fax: 86 21 50801922
 Email: hanzq@tigr.sh.cn

Monomials: $1, x, x^2, \dots, x^{n-1}$; Polynomials: $1, x, x^2, \dots, x^n$; Homomorphisms: $\text{Hom}(V, W)$.

1 (base) 10 769)

[illegible]

us-09-479-862-6.rni

Thu Aug 2 10:26:59 2001

```

1 IDENTIFICATION METHOD: S
US-08-884-424-6

Query Match 100.0% Score 12: 108 4: Length 12:
Best Local Similarity 100.0% Prod. No. 1,999,022:
Matches 12: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CTGAAGATGATG 12
111111111111
10 1 CTGAAGATGATG 12

RESULT 2
US-08-881-784-087C
Sequence 38, Application US/0881784
Patent No. 6084741
GENERAL INFORMATION:
APPLICANT: Crocon, Rodney B.
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE PREPARATION OF LIMONENE HYDROXYLASES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compat 386
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent in Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: B5,999,022
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DECKET NUMBER: WSK19777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 224-0718
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..19
OTHER INFORMATION: /product "Sequencing Primer S17 1P2"
US-08-881-784-48

Query Match 100.0% Score 12: 108 4: Length 19:
Best Local Similarity 100.0% Prod. No. 200,027:
Matches 12: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CTGAAGATGATG 12
111111111111
10 18 CTGAAGATGATG 7

RESULT 3
US-09-292-768-497C
Sequence 39, Application US/09292768
Patent No. 609185
GENERAL INFORMATION:
APPLICANT: Crocon, Rodney B.
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PREPARATION OF
TITLE OF INVENTION: LIMONENE HYDROXYLASES
FILE REFERENCE: WSK14463
CURRENT APPLICATION NUMBER: 09/292,768
EARLIER FILING DATE: 1999 04 14
EARLIER APPLICATION NUMBER: 09/081,784
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 39
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer 11
NAME/KEY: misc feature
LOCALIZATION: (1)-(19)
OTHER INFORMATION: sequencing primer
US-09-292-768-49

Query Match 100.0% Score 12: 108 4: Length 19:
Best Local Similarity 100.0% Prod. No. 200,027:
Matches 12: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CTGAAGATGATG 12
111111111111
10 18 CTGAAGATGATG 7

RESULT 4
US-09-292-768-497C
Sequence 40, Application US/09199910
Patent No. 5950047
GENERAL INFORMATION:
APPLICANT: Metcalf, Carol
TITLE OF INVENTION: Colipomucelides With Anti-Epstein
TITLE OF INVENTION: Barr Virus Activity
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lippin, S. Kusnet
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compat 386
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,510
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kotter, Ann Louise
REGISTRATION NUMBER: 43,924
REFERENCE/DECKET NUMBER: HYZ 017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 430-1300
TELEFAX: 617 430-1341
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs

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1 TYPE: nucleic acid
 2 STRANDNESS: single
 3 TOPOLOGY: linear
 4 MOLECULE TYPE: DNA
 5 HYPOTHETICAL: NO
 6 ANTI-SENSE: YES
 7
 8 US-09-479-862-6

Query Match 100.0% Score 12: 196 20 Length 207
 Best Local Similarity 100.0% Pred. No. 20-02
 Matches 12: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CUGAAGATGATG 12
 DB 12 CUGAAGATG 1

RESULT 5
 US-09-479-862-6 2/6
 1 Sequence 2: Application US/08-284122
 2 Patent No. 587854
 3 GENERAL INFORMATION:
 4 APPLICANT: Mulder, Carol
 5 TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-EPSTEIN-BARR
 6 VIRUS ACTIVITY
 7 NUMBER OF SEQUENCES: 63
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Fish & Richardson P.C.
 10 STREET: 225 Franklin Street
 11 CITY: Boston
 12 STATE: MA
 13 COUNTRY: USA
 14 ZIP: 02110-2804
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: Floppy disk
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: Patent In Release #1.0, Version #1.30
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: 09/094284122
 22 FILING DATE:
 23 CLASSIFICATION: 514
 24 ALTERNATE/AGENT INFORMATION:
 25 NAME: Fasso, J. Peter
 26 REGISTRATION NUMBER: 42,984
 27 REFERENCE/SEQUENCE NUMBER: 01,207,004-101
 28 TELECOMMUNICATION INFORMATION:
 29 TELEPHONE: 617/542-5070
 30 TELEFAX: 617/542-8906
 31 TELEX: 200154
 32 INFORMATION FOR SEQ ID NO: 2:
 33 SEQUENCE CHARACTERISTICS:
 34 LENGTH: 20 base pairs
 35 TYPE: nucleic acid
 36 STRANDNESS: single
 37 TOPOLOGY: linear
 38 MOLECULE TYPE: DNA
 39 US-09-479-862-6

Query Match 100.0% Score 12: 196 20 Length 207
 Best Local Similarity 100.0% Pred. No. 20-02
 Matches 12: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CUGAAGATGATG 12
 DB 12 CUGAAGATG 1

RESULT 6
 PCT-US-95-02082-2/6
 1 Sequence 2: Application US/95-02082

2 GENERAL INFORMATION:
 3 APPLICANT: Mulder, Carol
 4 TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-EPSTEIN-BARR
 5 VIRUS ACTIVITY
 6 NUMBER OF SEQUENCES: 3
 7 CORRESPONDENCE ADDRESS:
 8 ADDRESSEE: Lippin & Kosmer
 9 STREET: 200 State Street
 10 CITY: Boston
 11 STATE: Massachusetts
 12 COUNTRY: USA
 13 ZIP: 02109
 14 COMPUTER READABLE FORM:
 15 MEDIUM TYPE: Floppy disk
 16 COMPUTER: IBM PC compatible
 17 OPERATING SYSTEM: PC-DOS/MS-DOS
 18 SOFTWARE: Patent In Release #1.0, Version #1.25
 19 CURRENT APPLICATION DATA:
 20 APPLICATION NUMBER: 09/094284122
 21 FILING DATE:
 22 CLASSIFICATION:
 23 ALTERNATE/AGENT INFORMATION:
 24 NAME: Kerner, Ann-Louise
 25 REGISTRATION NUMBER: 34,524
 26 REFERENCE/SEQUENCE NUMBER: 017001
 27 TELECOMMUNICATION INFORMATION:
 28 TELEPHONE: 617-430-1400
 29 TELEFAX: 617-430-1411
 30 INFORMATION FOR SEQ ID NO: 2:
 31 SEQUENCE CHARACTERISTICS:
 32 LENGTH: 20 base pairs
 33 TYPE: nucleic acid
 34 STRANDNESS: single
 35 TOPOLOGY: linear
 36 MOLECULE TYPE: DNA
 37 HYPOTHETICAL: NO
 38 ANTI-SENSE: YES
 39 PCT US95-02082 2

Query Match 100.0% Score 12: 196 20 Length 207
 Best Local Similarity 100.0% Pred. No. 20-02
 Matches 12: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CUGAAGATGATG 12
 DB 12 CUGAAGATG 1

RESULT 7
 US-09-479-862-6 1/6
 1 Sequence 1: Application US/08199510
 2 Patent No. 5550047
 3 GENERAL INFORMATION:
 4 APPLICANT: Mulder, Carol
 5 TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-EPSTEIN-BARR
 6 VIRUS ACTIVITY
 7 NUMBER OF SEQUENCES: 4
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Lippin & Kosmer
 10 STREET: 200 State Street
 11 CITY: Boston
 12 STATE: Massachusetts
 13 COUNTRY: USA
 14 ZIP: 02109
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: Floppy disk
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: Patent In Release #1.0, Version #1.25
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08199510
 22 FILING DATE:

us-09-479-862-6.rni

Thu Aug 2 10:26:59 2001

```

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohnert, Ann Louise
REGISTRATION NUMBER: 43,924
REFERENCE/EXCERPT NUMBER: HY2 017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-430-1400
TELEFAX: 617-430-1411
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08 199 510-1

Query Match 100.00; Score 12; 106 2; Length 25;
Best Local Similarity 100.00; Prod. No. 200025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCGAAGATGAG 12
DB 20 CTCGAAGATGAG 9

RESULT 8
US-08 628 422-1/3
Sequence 1, Application US/08628422
Patent No. 5847854
GENERAL INFORMATION:
APPLICANT: Mulder, Carol
TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-EPSTEIN BARR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08628422
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fasso, J. Peter
REGISTRATION NUMBER: 42,984
REFERENCE/EXCERPT NUMBER: 040207094001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6A:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08 628 422-63

Query Match 100.00; Score 12; 106 2; Length 25;
Best Local Similarity 100.00; Prod. No. 200025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCGAAGATGAG 12
DB 6 CTCGAAGATGAG 17

RESULT 10
US-08 628 422-1/2
Sequence 1, Application PC/PUS96020042
GENERAL INFORMATION:
APPLICANT: Mulder, Carol
TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-EPSTEIN BARR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lippitt & Kusner
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts

```

```

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohnert, Ann Louise
REGISTRATION NUMBER: 43,924
REFERENCE/EXCERPT NUMBER: HY2 017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-430-1400
TELEFAX: 617-430-1411
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08 199 510-1

Query Match 100.00; Score 12; 106 2; Length 25;
Best Local Similarity 100.00; Prod. No. 200025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCGAAGATGAG 12
DB 20 CTCGAAGATGAG 9

RESULT 8
US-08 628 422-1/3
Sequence 1, Application US/08628422
Patent No. 5847854
GENERAL INFORMATION:
APPLICANT: Mulder, Carol
TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-EPSTEIN BARR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08628422
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fasso, J. Peter
REGISTRATION NUMBER: 42,984
REFERENCE/EXCERPT NUMBER: 040207094001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08 628 422-1

Query Match 100.00; Score 12; 106 2; Length 25;

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1  COUNTRY: USA
2  ZIP: 02109
3  COMPUTER READABLE FORM:
4  MEDIUM TYPE: Floppy disk
5  COMPUTER: IBM PC compatible
6  OPERATING SYSTEM: PC DOS/MS DOS
7  SOFTWARE: Patent in Release #1.0, Version #1.25
8  CURRENT APPLICATION DATA:
9  APPLICATION NUMBER: 02/095/02082
10 FILING DATE:
11 CLASSIFICATION:
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Forster, Ann Louise
14 REGISTRATION NUMBER: 33,523
15 REFERENCE/DOCKET NUMBER: 02/017001
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: 617-330-1100
18 TELEFAX: 617-330-1211
19 INFORMATION FOR SEQ ID NO: 1:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 25 base pairs
22 TYPE: nucleic acid
23 STRANDEDNESS: single
24 TOPOLOGY: linear
25 MOLECULE TYPE: cDNA
26 HYPOTHETICAL: NO
27 ANTI-SENSE: YES
28 PCT US95-02082-1

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Query Match 100.0% Score 12; DB 5; Length 25;
Best local similarity 100.0% Pct. No. 20-021
Matches 12; Conservative 0; Mismatches 0; Gaps 0;

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00 1 CTGAAGATGAG 12
1111111111
16 20 CTGAAGATGAG 9

```

```

RESULT 11
US-08-799-464A-12
Sequence 12, Application 05/0825946A
Patent No. 5998601
GENERAL INFORMATION:
APPLICANT: Martandh, Michael P. et al.
TITLE OF INVENTION: VR 2342 VIRAL NUCLEOTIDE SEQUENCE AND
METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: John M. Collins
STREET: 2405 Grand Blvd., Suite 400
CITY: Kansas City
STATE: Missouri
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02/095/02082
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 546
APPLICATION NUMBER: 08/247,543
FILING DATE: August 5, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 22007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050

```

```

1  TELEFAX: (816) 474-9057
2  INFORMATION FOR SEQ ID NO: 12:
3  SEQUENCE CHARACTERISTICS:
4  LENGTH: 369 base pairs
5  TYPE: nucleic acid
6  CHARGEDNESS: double
7  TOPOLOGY: linear
8  MOLECULE TYPE: cDNA
9  FEATURES:
10 NAME/KEY: CDS
11 LOCATION: 1..369
12 IDENTIFICATION METHOD: experimental
13 OTHER INFORMATION: /evidence EXPERIMENTAL
14 OTHER INFORMATION: /standard_name "VR 2342 chr 7"
15 US 08-799-464A-12

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Query Match 100.0% Score 12; DB 2; Length 369;
Best local similarity 100.0% Pct. No. 270-021
Matches 12; Conservative 0; Mismatches 0; Gaps 0;

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00 1 CTGAAGATGAG 12
1111111111
16 176 CTGAAGATGAG 187

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RESULT 12
PCT US95-09927-12
Sequence 12, Application 02/095/09927
GENERAL INFORMATION:
APPLICANT: Martandh, Michael P.
TITLE OF INVENTION: VR 2342 VIRAL NUCLEOTIDE SEQUENCE AND
METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: John M. Collins
STREET: 1101 Walnut, Suite 1400
CITY: Kansas City
STATE: Missouri
COUNTRY: USA
ZIP: 64106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02/095/09927
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,122
REFERENCE/DOCKET NUMBER: 22007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURES:
NAME/KEY: CDS
LOCATION: 1..369
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence EXPERIMENTAL
OTHER INFORMATION: /standard_name "VR 2342 chr 7"
PCT US95-09927-12

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RESULT 15

US-09-855-526B-14
 ? Sequence 14: Application US/09855526B
 ? Patent No. 6251404
 ? GENERAL INFORMATION:
 ? APPLICANT: DEEM, PAUL S.
 ? APPLICANT: BALBOK, PAUL R. G.
 ? APPLICANT: MENG, XIANG JIN
 ? APPLICANT: LOM, MELISSA A.
 ? APPLICANT: LYOO, YOUNG S.
 ? TITLE OF INVENTION: VACCINES AGAINST AN EBEN-LOCAL
 ? TITLE OF INVENTION: RESPONSE AGAINST VIRUSES CAUSING PERSISTENT RESPIRATORY AND
 ? TITLE OF INVENTION: REPRODUCTIVE DISEASES, METHODS OF PREVENTING A DISEASE
 ? TITLE OF INVENTION: A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE
 ? NUMBER OF SEQUENCES: 47
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: OBLON, SPIVAK, MUELLER, MATER & NEUSIADT,
 ? ADDRESSEE: P.C.
 ? STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 ? CITY: ARLINGTON
 ? STATE: VA
 ? COUNTRY: USA
 ? ZIP: 22202
 ? COMPUTER READABLE FORM:
 ? MEDIA TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC DOS/MS DOS
 ? SOFTWARE: Patent to Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: 09/098555-526B
 ? FILING DATE: 13-MAY-1997
 ? CLASSIFICATION: 424
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/969,071
 ? FILING DATE: 30-Oct-1992
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: LAVALLEY, JEAN-PAUL, M.P.
 ? REGISTRATION NUMBER: 41,451
 ? REFERENCE/DOCKET NUMBER: 4425-040 55X 51V
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 703-413-4000
 ? TELEFAX: 703-413-2220
 ? TELEX: 248855 GRAT DR
 ? INFORMATION FOR SEQ ID NO: 14:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 372 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: unknown
 ? TOPOLOGY: unknown
 ? MOLECULE TYPE: cDNA
 ? ORIGINAL SOURCE:
 ? ORGANISM: Porcine reproductive and respiratory syndrome
 ? ORGANISM: Virus
 ? STRAIN: Iowa
 ? INDIVIDUAL ISOLATE: IS0 12
 ? US 09 855-526B-14

Query Match 100.0% Score 127 Job 4 Length 472
 Best Local Similarity 100.0% Pct. No. 2,700-02
 Matches 12 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Q7 1 CTGAGAGATG 12
 |||||
 DB 176 CTGAGATGATG 187

Search completed: August 2, 2001, 07:12:41
 Job time: 7847 sec

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in financial matters. The text outlines various methods for organizing and storing data, including digital databases and physical filing systems. It also mentions the need for regular audits and reviews to ensure the integrity of the information.

2. The second part of the document focuses on the role of communication in achieving organizational goals. It highlights the importance of clear and concise communication, both internally and externally. The text provides guidelines for effective communication, such as using appropriate language, listening actively, and providing feedback. It also discusses the importance of maintaining open lines of communication and fostering a collaborative environment.

3. The third part of the document addresses the issue of risk management. It explains that identifying and assessing potential risks is a critical component of any strategic plan. The text describes various risk assessment tools and techniques, such as SWOT analysis and risk matrices. It also emphasizes the importance of developing contingency plans and implementing risk mitigation strategies to minimize the impact of potential threats.

4. The fourth part of the document discusses the importance of innovation and creativity in driving organizational growth. It encourages employees to think outside the box and explore new ideas and solutions. The text provides examples of innovative practices and strategies that have led to successful outcomes. It also mentions the importance of fostering a culture of innovation and providing the necessary resources and support for creative endeavors.

5. The fifth part of the document focuses on the importance of employee development and training. It explains that investing in the growth and development of employees is essential for long-term success. The text outlines various training and development programs, including on-the-job training, workshops, and seminars. It also emphasizes the importance of providing ongoing support and encouragement to employees throughout their development process.

6. The sixth part of the document discusses the importance of maintaining a strong corporate culture. It explains that a well-defined and consistent corporate culture can significantly impact an organization's performance and reputation. The text provides guidelines for developing and maintaining a strong corporate culture, such as clearly defining values and mission statements, and ensuring that all employees understand and embrace the organization's culture.

7. The seventh part of the document addresses the issue of sustainability and environmental responsibility. It explains that organizations have a responsibility to minimize their environmental impact and promote sustainable practices. The text outlines various strategies for achieving sustainability, such as reducing energy consumption, recycling, and using sustainable materials. It also mentions the importance of reporting on sustainability efforts and engaging with stakeholders on these issues.

8. The eighth part of the document discusses the importance of maintaining accurate financial records and reporting. It emphasizes that financial transparency is essential for building trust and credibility with investors and other stakeholders. The text outlines various financial reporting standards and practices, such as GAAP and IFRS. It also mentions the importance of conducting regular financial audits and reviews to ensure the accuracy of the information.

9. The ninth part of the document focuses on the importance of maintaining a strong legal and regulatory framework. It explains that organizations must comply with all applicable laws and regulations to avoid legal consequences. The text provides guidelines for developing and maintaining a strong legal and regulatory framework, such as consulting with legal counsel and staying up-to-date on changes in the law.

10. The tenth part of the document discusses the importance of maintaining a strong reputation and brand. It explains that a well-known and respected brand can significantly impact an organization's success. The text outlines various strategies for building and maintaining a strong reputation and brand, such as providing high-quality products and services, and engaging in social responsibility activities.

PI to produce trans carved and trans isopiperitenol

PS Example 5; Page 31; 80pp; English.

XX The invention relates to nucleotide sequences encoding spearmint

CC (-) limonene-6-hydroxylase (L6H) and peppermint (-) limonene 6-

CC hydroxylase (L4H). Host cells containing a vector comprising the

CC nucleotide sequences can be used for the recombinant production of

CC limonene hydroxylases or of primary enzyme products. The primary enzyme

CC products are trans-carved in the case of (-)-L6H or

CC trans isopiperitenol in the case of (-)-L4H, which are of subsequent use,

CC to obtain enhanced expression of limonene hydroxylase in plants to attain

CC enhanced trans carved or trans-isopiperitenol production as a precursor

CC or pathogen defense mechanism, attractant or environmental signal. The

CC limonene hydroxylase cDNAs also provide a useful tool for isolating

CC other monoterpene hydroxylase genes and for characterizing the regulation

CC of monoterpene biosynthesis. Sequences AAX06574-604 represent

CC (-)-limonene 6-hydroxylase cDNA sequences and primers which were also

CC used to construct the cDNA hybridisation probe III 2 (AAX06562).

XX

SQ Sequence 19 BP; 5 A; 7 C; 4 G; 4 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 12; 108 12; Length 19;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gap 0;

QY 1 CCGAAGATGATG 12
DB 18 CCGAAGATGATG 7
K33633 3
AA041541/2
13 AA041541 standard; DNA; 20 BP.
XX
XX AA041541;
XX
XX 10-AUG 1993 (first entry)
XX
XX Antisense oligomer targeting ZLF 1 AUG site.
XX
XX Epstein Barr virus; EBV; hybridisation; and isense modulation;
KW replication; nasopharyngeal carcinoma; Burkitt lymphoma; Epstein Barr
KW syndrome; infectious mononucleosis; latent; active; infectious;
XX
XX Synthetic.
XX
XX W09307802 A.
XX
XX 29 APR 1993.
XX
XX 24 OCT 1992; 92WO 0508989.
XX
XX 25 OCT 1991; 91US 0784605.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Anderson KP; Ecker DJ;
XX
XX W111193; 1121717B.
XX
XX oligonucleotide(s) hybridising with RNA of Epstein Barr virus
PI for treating active, latent and chronic EBV infections and
PI associated diseases e.g. nasopharyngeal carcinoma, Burkitt's
PI lymphoma
XX
XX claim 1; Page 20; 45pp; English.
XX
XX The synthetic peptide is an antisense modulator of Epstein Barr
CC virus and protein, contains at least one phosphorothioate linkage at
CC and modifications in the 2' position. These modifications improve
CC penetration into regions of the cell that contain nucleic acid and
CC also resistance to degradation by nucleases. The oligonucleotide
CC targets the AUG site of ZLF-1 and hybridises, thus
CC inhibiting replication of EBV. The oligomer may be used for
CC treating or preventing EBV-associated diseases, e.g. nasopharyngeal
CC carcinoma, Burkitt's lymphoma, Sjogren's syndrome, infectious
CC mononucleosis etc. The oligomer is effective against both latent and
CC active EBV infection.
XX
XX See also AA040575 9 and AA041517 44.
XX
SQ Sequence 20 BP; 6 A; 6 C; 4 G; 5 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 12; 108 14; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gap 0;

QY 1 CCGAAGATGATG 12
DB 15 CCGAAGATGATG 4

RESULT 2

AAF76648/c

ID AAF76648 standard; DNA; 19 BP.

XX

AC AAF76648;

XX

XX 15 MAY 2001 (first entry)

XX

DE Spearmint Limonene hydroxylase; L6H primer; SEQ ID NO. 19.

XX

XX Spearmint; peppermint; (-) limonene 6-hydroxylase

KW (-) limonene-3-hydroxylase; flavonoid; alcohol; poly phenol; see

XX

XX Mentha spicata.

XX

XX 056194185 R1.

XX

XX 27-FEB-2001.

XX

XX 14-APR-1999; 99US-0292768.

XX

XX 24-JUN-1997; 97US-0881784.

XX

XX (UNIV) UNIV WASHINGTON STATE RES FOUND.

XX

XX Croctean RB; Lupion SL; Karp F;

XX

XX WP1; 2001 244405/25.

XX

XX Recombinant limonene hydroxylase cDNA (L6H) for use in cell culture and

PI useful for altering production of limonene-6-hydroxylase or

PI limonene-3-hydroxylase in suitable host cell

XX

PS Example 5; Column 63; 57pp; English.

XX

XX the present invention provides the protein and coding sequences of the

CC peppermint and spearmint (-) limonene 3-hydroxylase and the spearmint

CC (-) limonene 6-hydroxylase. Also provided are a number of primers and PCR

CC primers which were used to isolate the sequences. These are useful in the

CC production of transgenic plants with altered flavor and aroma.

XX

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OS      Synthetic.
XX      Epstein Barr virus.
XX      W99747669-A1.
XX      16 OCT-1997.
XX      04-APR-1997; 97WO-0506104.
XX      05-APR-1997; 9803-0529422.
XX      (AYMA ) ENTV MASSACHUSETTS.
XX      Mulder C.
XX      W91; 1997 512404/47.
XX      Antisense oligonucleotide(s) that inhibit Epstein Barr virus
XX      function - used to treat or prevent EB virus infections, including
XX      tumours
XX      Disclosure: Page 51; 79pp; English.
XX      This antisense oligonucleotide is specific to a portion of the Bcl-1
XX      gene. Antisense oligonucleotides specific to any of the different
XX      strains of Epstein-Barr virus (EBV) such as the B2LF1, B2LF1.1, B2LF1.2,
XX      B2LF1.3, B2LF1.4, B2LF1.5, B2LF1.6, B2LF1.7, B2LF1.8, B2LF1.9, B2LF1.10,
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XX      B2LF1.714, B2LF1.715, B2LF1.716, B2LF1.717, B2LF1.718, B2LF1.719,
XX      B2LF1.720, B2LF1.721, B2LF1.722, B2LF1.723, B2LF1.724, B2LF1.725,
XX      B2LF1.726, B2LF1.727, B2LF1.728, B2LF1.729, B2LF1.730, B2LF1.731,
XX      B2LF1.732, B2LF1.733, B2LF1.734, B2LF1.735, B2LF1.736, B2LF1.737,
XX      B2LF1.738, B2LF1.739, B2LF1.740, B2LF1.741, B2LF1.742, B2LF1.743,
XX      B2LF1.744, B2LF1.745, B2LF1.746, B2LF1.747, B2LF1.748, B2LF1.749,
XX      B2LF1.750, B2LF1.751, B2LF1.752, B2LF1.753, B2LF1.754, B2LF1.755,
XX      B2LF1.756, B2LF1.757, B2LF1.758, B2LF1.759, B2LF1.760, B2LF1.761,
XX      B2LF1.762, B2LF1.763, B2LF1.764, B2LF1.765, B2LF1.766, B2LF1.767,
XX      B2LF1.768, B2LF1.769, B2LF1.770, B2LF1.771, B2LF1.772, B2LF1.773,
XX      B2LF1.774, B2LF1.775, B2LF1.776, B2LF1.777, B2LF1.778, B2LF1.779,
XX      B2LF1.780, B2LF1.781, B2LF1.782, B2LF1.783, B2LF1.784, B2LF1.785,
XX      B2LF1.786, B2LF1.787, B2LF1.788, B2LF1.789, B2LF1.790, B2LF1.791,
XX      B2LF1.792, B2LF1.793, B2LF1.794, B2LF1.795, B2LF1.796, B2LF1.797,
XX      B2LF1.798, B2LF1.799, B2LF1.800, B2LF1.801, B2LF1.802, B2LF1.803,
XX      B2LF1.804, B2LF1.805, B2LF1.806, B2LF1.807, B2LF1.808, B2LF1.809,
XX      B2LF1.810, B2LF1.811, B2LF1.812, B2LF1.813, B2LF1.814, B2LF1.815,
XX      B2LF1.816, B2LF1.817, B2LF1.818, B2LF1.819, B2LF1.820, B2LF1.821,
XX      B2LF1.822, B2LF1.823, B2LF1.824, B2LF1.825, B2LF1.826, B2LF1.827,
XX      B2LF1.828, B2LF1.829, B2LF1.830, B2LF1.831, B2LF1.832, B2LF1.833,
XX      B2LF1.834, B2LF1.835, B2LF1.836, B2LF1.837, B2LF1.838, B2LF1.839,
XX      B2LF1.840, B2LF1.841, B2LF1.842, B2LF1.843, B2LF1.844, B2LF1.845,
XX      B2LF1.846, B2LF1.847, B2LF1.848, B2LF1.849, B2LF1.850, B2LF1.851,
XX      B2LF1.852, B2LF1.853, B2LF1.854, B2LF1.855, B2LF1.856, B2LF1.857,
XX      B2LF1.858, B2LF1.859, B2LF1.860, B2LF1.861, B2LF1.862, B2LF1.863,
XX      B2LF1.864, B2LF1.865, B2LF1.866, B2LF1.867, B2LF1.868, B2LF1.869,
XX      B2LF1.870, B2LF1.871, B2LF1.872, B2LF1.873, B2LF1.874, B2LF1.875,
XX      B2LF1.876, B2LF1.877, B2LF1.878, B2LF1.879, B2LF1.880, B2LF1.881,
XX      B2LF1.882, B2LF1.883, B2LF1.884, B2LF1.885, B2LF1.886, B2LF1.887,
XX      B2LF1.888, B2LF1.889, B2LF1.890, B2LF1.891, B2LF1.892, B2LF1.893,
XX      B2LF1.894, B2LF1.895, B2LF1.896, B2LF1.897, B2LF1.898, B2LF1.899,
XX      B2LF1.900, B2LF1.901, B2LF1.902, B2LF1.903, B2LF1.904, B2LF1.905,
XX      B2LF1.906, B2LF1.907, B2LF1.908, B2LF1.909, B2LF1.910, B2LF1.911,
XX      B2LF1.912, B2LF1.913, B2LF1.914, B2LF1.915, B2LF1.916, B2LF1.917,
XX      B2LF1.918, B2LF1.919, B2LF1.920, B2LF1.921, B2LF1.922, B2LF1.923,
XX      B2LF1.924, B2LF1.925, B2LF1.926, B2LF1.927, B2LF1.928, B2LF1.929,
XX      B2LF1.930, B2LF1.931, B2LF1.932, B2LF1.933, B2LF1.934, B2LF1.935,
XX      B2LF1.936, B2LF1.937, B2LF1.938, B2LF1.939, B2LF1.940, B2LF1.941,
XX      B2LF1.942, B2LF1.943, B2LF1.944, B2LF1.945, B2LF1.946, B2LF1.947,
XX      B2LF1.948, B2LF1.949, B2LF1.950, B2LF1.951, B2LF1.952, B2LF1.953,
XX      B2LF1.954, B2LF1.955, B2LF1.956, B2LF1.957, B2LF1.958, B2LF1.959,
XX      B2LF1.960, B2LF1.961, B2LF1.962, B2LF1.963, B2LF1.964, B2LF1.965,
XX      B2LF1.966, B2LF1.967, B2LF1.968, B2LF1.969, B2LF1.970, B2LF1.971,
XX      B2LF1.972, B2LF1.973, B2LF1.974, B2LF1.975, B2LF1.976, B2LF1.977,
XX      B2LF1.978, B2LF1.979, B2LF1.980, B2LF1.981, B2LF1.982, B2LF1.983,
XX      B2LF1.984, B2LF1.985, B2LF1.986, B2LF1.987, B2LF1.988, B2LF1.989,
XX      B2LF1.990, B2LF1.991, B2LF1.992, B2LF1.993, B2LF1.994, B2LF1.995,
XX      B2LF1.996, B2LF1.997, B2LF1.998, B2LF1.999, B2LF1.1000, B2LF1.1001,
XX      B2LF1.1002, B2LF1.1003, B2LF1.1004, B2LF1.1005, B2LF1.1006, B2LF1.1007,
XX      B2LF1.1008, B2LF1.1009, B2LF1.1010, B2LF1.1011, B2LF1.1012, B2LF1.1013,
XX      B2LF1.1014, B2LF1.1015, B2LF1.1016, B2LF1.1017, B2LF1.1018, B2LF1.1019,
XX      B2LF1.1020, B2LF1.1021, B2LF1.1022, B2LF1.1023, B2LF1.1024, B2LF1.1025,
XX      B2LF1.1026, B2LF1.1027, B2LF1.1028, B2LF1.1029, B2LF1.1030, B2LF1.1031,
XX      B2LF1.1032, B2LF1.1033, B2LF1.1034, B2LF1.1035, B2LF1.1036, B2LF1.1037,
XX      B2LF1.1038, B2LF1.1039, B2LF1.1040, B2LF1.1041, B2LF1.1042, B2LF1.1043,
XX      B2LF1.1044, B2LF1.1045, B2LF1.1046, B2LF1.1047, B2LF1.1048, B2LF1.1049,
XX      B2LF1.1050, B2LF1.1051, B2LF1.1052, B2LF1.1053, B2LF1.1054, B2LF1.1055,
XX      B2LF1.1056, B2LF1.1057, B2LF1.1058, B2LF1.1059, B2LF1.1060, B2LF1.1061,
XX      B2LF1.1062, B2LF1.1063, B2LF1.1064, B2LF1.1065, B2LF1.1066, B2LF1.1067,
XX      B2LF1.1068, B2LF1.1069, B2LF1.1070, B2LF1.1071, B2LF1.1072, B2LF1.1073,
XX      B2LF1.1074, B2LF1.1075, B2LF1.1076, B2LF1.1077, B2LF1.1078, B2LF1.1079,
XX      B2LF1.1080, B2LF1.1081, B2LF1.1082, B2LF1.1083, B2LF1.1084, B2LF1.1085,
XX      B2LF1.1086, B2LF1.1087, B2LF1.1088, B2LF1.1089, B2LF1.1090, B2LF1.1091,
XX      B2LF1.1092, B2LF1.1093, B2LF1.1094, B2LF1.1095, B2LF1.1096, B2LF1.1097,
XX      B2LF1.1098, B2LF1.1099, B2LF1.1100, B2LF1.1101, B2LF1.1102, B2LF1.1103,
XX      B2LF1.1104, B2LF1.1105, B2LF1.1106, B2LF1.1107, B2LF1.1108, B2LF1.1109,
XX      B2LF1.1110, B2LF1.1111, B2LF1.1112, B2LF1.1113, B2LF1.1114, B2LF1.1115,
XX      B2LF1.1116, B2LF1.1117, B2LF1.1118, B2LF1.1119, B2LF1.1120, B2LF1.1121,
XX      B2LF1.1122, B2LF1.1123, B2LF1.1124, B2LF1.1125, B2LF1.1126, B2LF1.1127,
XX      B2LF1.1128, B2LF1.1129, B2LF1.1130, B2LF1.1131, B2LF1.1132, B2LF1.1133,
XX      B2LF1.1134, B2LF1.1135, B2LF1.1136, B2LF1.1137, B2LF1.1138, B2LF1.1139,
XX      B2LF1.1140, B2LF1.1141, B2LF1.1142, B2LF1.1143, B2LF1.1144, B2LF1.1145,
XX      B2LF1.1146, B2LF1.1147, B2LF1.1148, B2LF1.1149, B2LF1.1150, B2LF1.1151,
XX      B2LF1.1152, B2LF1.1153, B2LF1.1154, B2LF1.1155, B2LF1.1156, B2LF1.1157,
XX      B2LF1.1158, B2LF1.1159, B2LF1.1160, B2LF1.1161, B2LF1.1162, B2LF1.1163,
XX      B2LF1.1164, B2LF1.1165, B2LF1.1166, B2LF1.1167, B2LF1.1168, B2LF1.1169,
XX      B2LF1.1170, B2LF1.1171, B2LF1.1172, B2LF1.1173, B2LF1.1174, B2LF1.1175,
XX      B2LF1.1176, B2LF1.1177, B2LF1.1178, B2LF1.1179, B2LF1.1180, B2LF1.1181,
XX      B2LF1.1182, B2LF1.1183, B2LF1.1184, B2LF1.1185, B2LF1.1186, B2LF1.1187,
XX      B2LF1.1188, B2LF1.1189, B2LF1.1190, B2LF1.1191, B2LF1.1192, B2LF1.1193,
XX      B2LF1.1194, B2LF1.1195, B2LF1.1196, B2LF1.1197, B2LF1.1198, B2LF1.1199,
XX      B2LF1.1200, B2LF1.1201, B2LF1.1202, B2LF1.1203, B2LF1.1204, B2LF1.1205,
XX      B2LF1.1206, B2LF1.1207, B2LF1.1208, B2LF1.1209, B2LF1.1210, B2LF1.1211,
XX      B2LF1.1212, B2LF1.1213, B2LF1.1214, B2LF1.1215, B2LF1.1216, B2LF1.1217,
XX      B2LF1.1218, B2LF1.1219, B2LF1.1220, B2LF1.1221, B2LF1.1222, B2LF1.1223,
XX      B2LF1.1224, B2LF1.1225, B2LF1.1226, B2LF1.1227, B2LF1.1228, B2LF1.1229,
XX      B2LF1.1230, B2LF1.1231, B2LF1.1232, B2LF1.1233, B2LF1.1234, B2LF1.1235,
XX      B2LF1.1236, B2LF1.1237, B2LF1.1238, B2LF1.1239, B2LF1.1240, B2LF1.1241,
XX      B2LF1.1242, B2LF1.1243, B2LF1.1244, B2LF1.1245, B2LF1.1246, B2LF1.
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Thu Aug 2 10:26:58 2001

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PR 19 DEC-1996: 96DS-0769951.
XX (ISIS-) ISIS PHARM INC.
PA Chen D, Cole DL, Srivatsa GS;
XX WFL 1998 4292271.
XX Matrix for selective separation of oligonucleotide, useful for,
PI e.g., large scale purification of antisense agents from their
PI deletion derivatives formed during synthesis
XX Disclosure, Page 152: 18pp; English.
XX AAX24663 268 represent oligonucleotides which can be purified using the
XX method of the invention. The specification describes a matrix that
XX comprises a support and an affinity unit that specifically and
XX reversibly binds a target oligonucleotide, and comprises a sequence of
XX bases having the reverse complement of a hybridising portion of the
XX target oligonucleotide. The matrix is used for affinity purification of
XX synthetic oligonucleotides, specifically antisense agents, for treatment
XX of hyperproliferative diseases, e.g., Alzheimer's, for modulating
XX expression of cell surface proteins, and to inhibit a eukaryotic
XX pathogen, retrovirus or other viruses.
XX Sequence 20 BP; 8 A; 5 C; 2 G; 5 T; 0 other;
SQ

Query Match 100.0%; Score 12; DB 19; Length 20;
Best Local Similarity 100.0%; Prod. No. 7,96,002;
Matches 12; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

QY 1 CTGAAGATGATG 12
DB 12 CTGAAGATGATG 1

RESULT 7
AAX24663
ID AAX24663 standard; DNA; 20 BP.
XX AAX24663;
AC AAX24663;
XX 18-JUN-1999 (first entry)
XX deletion sequence oligonucleotide 116.
XX deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
XX probe; cellular adhesion modulator; cellular proliferation modulator;
XX human retrovirus; human immunodeficiency virus; non-human retrovirus;
XX HIV; primer; SS.
XX Synthetic.
XX W09911820-A1.
XX 11-MAR-1999.
XX 01-SEP-1998; 98WO-US18084.
XX 02-SEP-1997; 97OS-0924771.
XX (ISIS-) ISIS PHARM INC.
XX Chen D, Srivatsa GS;
XX WFL 1999-205198/17.
XX New compositions comprising sensor arrays made up of unique probe
XX oligonucleotides - useful for characterizing a sample of target
XX deletion oligonucleotides

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PS Example 9; Page 108; 16pp; English.
XX This invention describes a novel composition comprising a number of
XX sensor arrays, where each array comprises a unique probe
XX oligonucleotide, which is the reverse complement of part of a unique
XX target oligonucleotide present in a mixture of target deletion or non-
XX oligonucleotides. The compositions form a method for characterizing a
XX sample of target deletion oligonucleotides which are labelled and
XX hybridize with the probe oligonucleotides of the sensor arrays. Each
XX oligonucleotide and their targets are represented in AAX, 049 X-000.
XX oligonucleotides characterized by the method form pharmaceutical
XX compositions that are useful for modulating cellular adhesion of
XX retrovirus, and being active against a eukaryotic pathogen, a human
XX retrovirus, a human immunodeficiency virus (HIV), or a non-human
XX retrovirus, including influenza virus, Epstein Barr virus, hepatitis
XX Syncytial virus or cytomegalovirus (CMV). The compositions enable
XX characterization of deletion sequence oligonucleotides having to do with
XX but different nucleobase sequences, and quantification of different
XX species of deletion sequence ("target") oligonucleotides in a mixture.
XX Also, if the specificity of the oligonucleotide's nucleobase sequence
XX for its reverse complement is not modified, the method may be performed
XX using oligodeoxynucleotides.
XX Sequence 20 BP; 8 A; 5 C; 2 G; 5 T; 0 other;
SQ

Query Match 100.0%; Score 12; DB 20; Length 20;
Best Local Similarity 100.0%; Prod. No. 7,96,002;
Matches 12; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

QY 1 CTGAAGATGATG 12
DB 12 CTGAAGATGATG 1

RESULT 8
AAX18784
ID AAX18784 standard; DNA; 20 BP.
XX AAX18784;
AC AAX18784;
XX 10 MAY 1999 (first entry)
XX Target Epstein Barr virus antisense oligonucleotide #116.
XX Cellular adhesion protein; proliferation; antisense oligonucleotide;
XX alimentary canal; transport; gastrointestinal mucosa; cancer;
XX Alzheimer's disease; beta-thalassemia; malaria; viral infection;
XX HIV; inflammation; SS.
XX Synthetic.
XX W09901579-A1.
XX 14-JAN-1999.
XX 01-JUL-1998; 98WO-US13574.
XX 01-JUL-1997; 97US-0886829.
XX (ISIS-) ISIS PHARM INC.
XX Barbee G, Long C;
XX WFL 1999 10607709.
XX Composition comprising nucleic acid and penetration enhancer, useful
XX particularly for delivering therapeutic antisense oligonucleotides
XX across the gastrointestinal mucosa, provides high bioavailability.
XX Example 2; Page 108; 115pp; English.
XX A pharmaceutical composition has been developed which comprises a
XX

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CC nucleic acid and at least one penetrant enhancer. The compositions are
 CC used: (i) to treat or prevent any disease or disorder, (ii) to be
 CC treated with the nucleic acid, (iii) to prevent, attenuate or eliminate
 CC beta-thalassemia, malaria, viral infections (including human immunodeficiency virus (HIV)), inflammation, to human or animal models,
 CC (iii) to investigate the role of a gene or gene product in non-human
 CC animals; and (iii) to modulate gene expression in cells, tissues or
 CC organs. The compositions provide bioavailability of at least 15,
 CC preferably 17-45%, the penetration enhancer improves: (i) transport of
 CC the nucleic acid across the mucosa of the alimentary canal and into
 CC cells; and (ii) increases stability of the nucleic acid. Oral
 CC administration avoids the complications and expense of intravenous or
 CC other methods of administration. AAX18669 to AAX18799 and AAX18801
 CC represent antisense oligonucleotide sequences which can be used as the nucleic
 CC acid in the method of the invention.

XX Sequence 20 BP; 8 A; 5 G; 2 C; 5 T; 0 other;

Query Match 100.0%; Score 12; DB 20; Length 20;
 Best Local Similarity 100.0%; Prod. No. 7.9e-02;
 Matches 12; Conservative 0; Mismatches 0; Gaps 0;

00 1 CTGAAGATGATG 12
 01 TTTTTTTTTT
 02 12 CTGAAGATGATG 1

RESULT 9
 AA243777
 ID AA243777 standard; DNA: 20 BP
 AC AA243777;
 XX
 XX 14 MAR 2000 (first entry)
 XX Epstein-Barr virus targeted antisense oligonucleotide (BY 10 42).
 XX
 XX Viral infection; expression; modulation; antisense;
 KW non-parenteral delivery; epitope; immunisation; oncogene;
 KW ulcerative colitis; Crohn's disease; inflammatory bowel disease;
 KW cellular proliferation; ss.

XX Synthetic.
 XX Epstein-Barr virus.
 XX W9960012-A1.

XX 25-NOV-1999. 9960-0811-094.
 XX 20-MAY-1999; 9960-0811-094.
 XX 21-MAY-1998; 9805-0082-24.

XX (ISIS-) LISTS PHARM INC

XX Tong C, Cook PB, Tillingham J, Bridges CP, Becker GJ, Huxford RM;
 XX WPI: 2000-0724-29/06.

XX New oligonucleotide compositions used for the non-parenteral delivery
 of anti-sense oligos, ribozymes, peptide nucleic acids, molecular
 decoys, external guide sequences or aptamers

XX Example 2, Page 129, 139pp, English.

XX Sequences AA243774-243803, AA243809 and AA243891 represent antisense
 oligonucleotides destined to have therapeutic activity against certain
 non-retroviral viruses. The invention relates to new compositions for
 the non-parenteral delivery of oligonucleotides comprising at
 least one oligonucleotide in an emulsion, oligonucleotides
 delivered via the compositions of the invention can be used to modulate
 expression of a cellular adhesion protein, modulate a rate of cellular

CC proliferation, or have biological activity against cytokinetic pathways
 CC in the digestive tract, they can be used for treating conditions including
 CC ulcerative colitis, Crohn's disease, inflammatory bowel disease
 CC or undue cellular proliferation. The compositions can enhance the local
 CC and systemic uptake and delivery of nucleic acids via non-parenteral
 CC routes of administration (e.g., via the alimentary canal, skin, eyes,
 CC pulmonary tract, urethra or vagina).

XX Sequence 20 BP; 8 A; 5 G; 2 C; 5 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 20;
 Best Local Similarity 100.0%; Prod. No. 7.9e-02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

00 1 CTGAAGATGATG 12
 01 TTTTTTTTTT
 02 12 CTGAAGATGATG 1

RESULT 10
 AA103757
 ID AA103757 standard; cDNA: 25 BP;
 AC AA103757;
 XX

XX 22 MAR 1996 (first entry)
 XX Synthetic oligonucleotide #1 hybridisable to BZLF1 RNA.
 XX BZLF1: Epstein Barr virus; EBV; therapy; ss.

XX Synthetic.

XX W9922554-A1.

XX 24 AUG 1995.

XX 17 FEB 1999; 95AW-0502082.

XX 18-FEB-1994; 94US-0199510.

XX (BYBR) HYBRIDON INC.

XX Mulder C;

XX WPI: 1995-02685/59.

XX oligonucleotide(s) having anti-Epstein Barr Virus activity in
 complementary to a portion of the BZLF1 RNA of EBV
 Claim 19; Page 31; 47pp; English.

XX The sequences represented by AA103757-59 are synthetic oligonucleotides
 that are complementary to and hybridisable with a portion of the BZLF1
 RNA of Epstein Barr Virus (EBV). BZLF1 is the first gene activated in
 the lytic cycle of EBV. This sequence is complementary to 25
 nucleotides of the region flanking the initiation codon. These sequences
 hybridise to the region of mRNA immediately surrounding the translational
 initiation codon and thereby prevent synthesis of BZLF1. These sequences
 can be altered to contain modified intermolecular linkages (e.g.,
 triphosphonate, phosphorothioate, carbamate, carbonate, phosphate,
 triester, and others) without compromising their ability to hybridise to
 BZLF1 mRNA. The sequences can be used in pharmaceutical compositions
 which inhibit the replication of EBV in a cell. The compositions can
 therefore be used in treatment of EBV infection.

XX Sequence 25 BP; 6 A; 6 G; 5 C; 8 T; 0 other;

Query Match 100.0%; Score 12; DB 16; Length 25;
 Best Local Similarity 100.0%; Prod. No. 8.1e-02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0;

QY 1 CTGAAGATGATG 12
 ID 1111111111
 DB 20 CTGAAGATGATG 9

RESULT 11

AA192694
 ID AA192694 standard; DNA; 25 BP.

XX AA192694;

XX 22-APR-1998 (first entry)

XX Sense sequence S25 of B2LF1 antisense oligonucleotide Z1.

XX Epstein-Barr virus; antisense oligonucleotide; EBV; treatment; tumour;

XX terminal protein; B2LF1, B2LF1, B2LF1; B2LF1; B2LF1;

XX B2LF2; B2LF2; sense sequence; SS.

XX Synthetic.

XX Epstein-Barr virus.

XX W09747669 A1.

XX 16-OCT-1997.

XX 04 APR 1997; 97W0-US06104.

XX 05 APR 1996; 96US-0628422.

XX (OYMA-) UNIV MASSACHUSETTS.

XX Muller C;

XX WPT; 1997 512405/47.

XX Antisense oligonucleotide(s) that inhibit Epstein Barr virus

XX function - used to treat or prevent EB virus infections, including

XX tumours

XX Disclosure; Page 64; 7pp; English.

XX This is the sense sequence of the antisense oligonucleotide Z1 specific
 CC to a portion of a B2LF1 gene. Antisense oligonucleotides specific to any
 CC of the different strains of Epstein Barr virus (EBV) such as the B2LF1,
 CC B2LF1, B2LF1, B2LF1, B2LF1, B2LF1, B2LF1, B2LF1, B2LF1 and terminal
 CC proteins 1 and 2 are used to inhibit EBV function. This S25 acts as a
 CC negative control in the synthesis of such antisense oligonucleotides. The
 CC antisense oligonucleotides are antisense sequences that inhibit EBV
 CC replication or gene expression. The antisense oligonucleotides of the
 CC vectors expressing them, are used to treat or prevent EBV infection
 CC (including tumours such as nasopharyngeal carcinoma) in mammals. When
 CC labelled, they can also be used to detect cells infected with EBV. The
 CC antisense oligonucleotides can be targeted to either the latent or the
 CC lytic phase of the virus cycle. Combinations of the antisense
 CC oligonucleotides directed against different viral genes may provide a
 CC synergistic inhibitory effect. Formulation of these antisense
 CC oligonucleotides with transfection agents can increase the efficiency
 CC and reduce their needed dosage.

XX Sequence 25 BP; 8 A; 5 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 12; DB 18; Length 25;

Best Local Similarity 100.0%; Pred. No. 3,1-032;

Matches 12; Conservation 0; Mismatches 0; Gaps 0;

QY 1 CTGAAGATGATG 12

DB 6 ctgaagatgatg 17

RESULT 12

AA192690/c

ID AA192690 standard; DNA; 25 BP.

XX AA192690;

XX 22-APR-1998 (first entry)

XX B2LF1 gene specific antisense oligonucleotide Z1.

XX Epstein Barr virus; antisense oligonucleotide; EBV; treatment; tumour;

XX B2LF1; B2LF1; B2LF1; B2LF1; B2LF1; B2LF1; B2LF1; B2LF1;

XX Synthetic.

XX Epstein Barr virus.

XX W09747669 A1.

XX 16-OCT-1997.

XX 04-APR-1997; 97W0-US06104.

XX 05 APR 1996; 96US-0628422.

XX (OYMA-) UNIV MASSACHUSETTS.

XX Muller C;

XX WPT; 1997 512405/47.

XX Antisense oligonucleotide(s) that inhibit Epstein Barr virus.

XX function - used to treat or prevent EB virus infections, including

XX tumours

XX Disclosure; Page 60; 7pp; English.

XX This antisense oligonucleotide is specific to a portion of the B2LF1
 CC gene. Antisense oligonucleotides specific to any of the different
 CC strains of Epstein Barr virus (EBV) such as the B2LF1, B2LF1, B2LF1,
 CC B2LF1, B2LF1, B2LF1, B2LF1, B2LF1, B2LF1, B2LF1 and terminal
 CC proteins 1 and 2 are used to inhibit EBV function. These antisense oligonucleotides are
 CC antisense sequences that inhibit EBV replication or gene expression. The
 CC antisense oligonucleotides of the vectors expressing them, are used to
 CC treat or prevent EBV infection (including tumours such as nasopharyngeal
 CC carcinoma) in mammals. When labelled, they can also be used to detect
 CC cells infected with EBV. The antisense oligonucleotides can be targeted
 CC to either the latent or the lytic phase of the virus cycle. Combinations
 CC of the antisense oligonucleotides directed against different viral genes
 CC may provide a synergistic inhibitory effect. Formulation of these
 CC antisense oligonucleotides with transfection agents can increase the
 CC efficiency and reduce their needed dosage.

XX Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 other;

Query Match 100.0%; Score 12; DB 18; Length 25;

Best Local Similarity 100.0%; Pred. No. 3,1-032;

Matches 12; Conservation 0; Mismatches 0; Gaps 0;

QY 1 CTGAAGATGATG 12

DB 20 CTGAAGATGATG 9

RESULT 14

AAV28261/c

ID AAV28261 standard; DNA; 25 BP.

XX AAV28261;

XX 08 OCT 1998 (first entry)

XX Antisense oligonucleotide to cytomegalovirus.

PA (ISIS-) ISIS PHARM INC.
XX
PI Bardee G, Teut C;
XX
DK WPI; 1999 106077/09.
XX
XX Composition comprising nucleic acid and penetration enhancer used
PI particularly for delivering therapeutic antisense oligonucleotides
PI across the gastrointestinal mucosa, provides high bioavailability
XX
XX Example 2; Page 108; 115pp; English.
XX
XX A pharmaceutical composition has been developed which comprises a
CC nucleic acid and at least one penetration enhancer. The compositions are
CC used: (i) to treat or prevent any disease or disorder that can be
CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
CC beta-thalassemia, malaria, viral infections (including human immune
CC deficiency virus (HIV)), inflammation, in human or animal medicine;
CC (ii) to investigate the role of a gene or gene product in non-human
CC animals; and (iii) to modulate gene expression in cells, tissues or
CC organs. The compositions provide bioavailability of at least 15,
CC preferably 17-35%. The penetration enhancer improves: (i) transport of
CC the nucleic acid across the mucosa of the alimentary canal and into
CC cells; and (ii) increases stability of the nucleic acid, oral
CC administration avoids the complications and expense of intravenous or
CC other methods of administration. AAX18669 to AAX18799 and AAX18801
CC represent antisense oligonucleotides which can be used as the nucleic
CC acid in the method of the invention.
XX
SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 other;

Query Match 100.0%; Score 12; PB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 8; Rev02;
Matches 12; Conservative 9; Mismatches 0; Gaps 0;
0Y 1 CTCACAGATG 12
DB 1111111111
20 CTCACAGATG 9

Search completed: August 2, 2001, 07:17:46
Job time: 804.2 sec

Genotool version 4.5
Copyright (c) 1993 - 2001, Compugen, Ltd.

EM Loci: nucleic search, using sw model

Run on: August 2, 2001, 06:08:00 : Search time: 47m 43 seconds
(without alignments)
29,863 Million cell updates/sec

Title: us-09-479-862-6
Project source: 12
Sequence: 1 CTGAAGATGATG 12

Scoring table: IDENTITY_NUC
Gapop 10.0 : Gapext 1.0

Searches: 10228115 seqs, 4726429750 residues 20456240
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: qb_est1: *
2: qb_est2: *
3: qb_est3: *
4: qb_est4: *
5: qb_est5: *
6: qb_est6: *
7: qb_est7: *
8: qb_est8: *
9: qb_est9: *
10: qb_est10: *
11: qb_est11: *
12: qb_est12: *
13: qb_est13: *
14: qb_est14: *
15: qb_est15: *
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17: qb_est17: *
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26: qb_est34: *
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28: qb_est35: *
29: qb_est37: *
30: qb_est38: *
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33: em_est3a: *
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100: em_est3a: *
101: em_est3a: *
102: qb_est25: *
103: qb_est26: *
104: qb_est27: *
105: qb_est28: *
106: qb_est29: *
107: qb_est30: *
108: qb_est31: *
109: qb_est32: *
110: qb_est33: *
111: qb_est34: *
112: qb_est35: *
113: qb_est36: *
114: qb_est37: *
115: qb_est38: *
116: qb_est39: *

us-09-479-862-6.rst

Thu Aug 2 10:27:00 2001

```

117: qb_est48:*
118: qb_est49:*
119: qb_est50:*
120: qb_est51:*
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140: qb_est71:*
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142: qb_est73:*
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184: qb_est115:*
185: qb_est116:*
186: qb_est117:*
187: qb_est118:*
188: qb_est119:*
189: qb_est120:*

```

Pred. No. is the number of results predicted by chance to be a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

BASE COUNT 17 a 12 c 20 g 18 t 2 others

Query Match
Best Local Similarity 100.00; Score 12; DB 9; Length 69;
Matches 12; Conserved 0; Mismatches 0; Gaps 0;

QY 1 CTGAAGATGATG 12
|||||
DB 35 CTGAAGATGATG 46

RESULT 3
AA553284
LOCUS
DEFINITION
Accession
Version
Keywords
Source
Organism
Reference
Authors
Title
Journal
Comment
Features
Source
Base Count
Origin

Query Match
Best Local Similarity 100.00; Score 12; DB 9; Length 76;
Matches 12; Conserved 0; Mismatches 0; Gaps 0;

QY 1 CTGAAGATGATG 12
|||||
DB 35 CTGAAGATGATG 46

BASE COUNT 17 a 12 c 20 g 18 t 2 others

Query Match
Best Local Similarity 100.00; Score 12; DB 9; Length 69;
Matches 12; Conserved 0; Mismatches 0; Gaps 0;

QY 1 CTGAAGATGATG 12
|||||
DB 35 CTGAAGATGATG 46

RESULT 3
AA553284
LOCUS
DEFINITION
Accession
Version
Keywords
Source
Organism
Reference
Authors
Title
Journal
Comment
Features
Source
Base Count
Origin

Query Match
Best Local Similarity 100.00; Score 12; DB 9; Length 76;
Matches 12; Conserved 0; Mismatches 0; Gaps 0;

QY 1 CTGAAGATGATG 12
|||||
DB 35 CTGAAGATGATG 46

[illegible]

Query Match 100.0% Score 12; DB 142; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAAGATGATG 12
 111111111111
 DB 83 CTGAAGATGATG 94

RESULT 15

AA212001 112 bp mRNA EST 31 JAN 1997
 mos9505.11 Bedlington mouse embryonic region Mus musculus cDNA
 clone IMAGE:560720 5' similar to IR:285987 5,255987 ORF, COMPLETE
 CDS, 1, mRNA sequence.

AA212001
 AA212001.1 31:1810655
 EST.
 house mouse.

Mus musculus
 ORGANISM

Pharyngota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurinae; Muridae; Mus;
 1 (bases 1 to 112)
 Marín, M., Billeter, A., Allen, M., Bakula, M., Bittich, N., Dubouche, L.,
 Geisel, S., Kucaba, T., Lucy, M., Le, M., Martin, J., Morris, M.,
 Schellander, K., Stapp, M., Tan, P., Underwood, K., Moore, R.,
 Theising, B., Wylie, L., Lemmon, G., Soares, R., Wilson, R. and
 Waterston, R.

The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Drive, Box 8001, St. Louis, Mo 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through ENIGMA; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 M11341512

Trace considered overall poor quality
 Possible reversed clone; similarity on wrong strand
 Seq primer: -28614 rev1 F1 from AmerSham
 High quality sequence stop: 1.

FEATURES

Location/Qualifiers
 1..112
 /organism "Mus musculus"
 /strain "mos9505.11 x 10A"
 /db_xref "taxon:10090"
 /clone "IMAGE:560720"
 /clone_lib "Bedlington mouse embryonic region"
 /sex "pooled"
 /tissue_type "embryo"
 /dev_stage "7.5dpc"
 /lab_host "PH125"
 /note "organ: whole embryo; Vector: pGEM-Simple; Site_1:
 Salt; Site_2: Not cloned unidirectionally. Primer:
 oligo df. Gastrulating embryos were collected at 7.5dpc
 from 0.5H6.6 x 10A matings, excluding embryos that had
 developed head folds and all extraembryonic tissues.
 Average insert size: 1.3 kb (range: 0.5 - 4.0 kb).
 Referenced in development 121, 2479-2485 (1995)".

BASE COUNT 29 a 26 c 28 g 29 t

ORIGIN

Query Match 100.0% Score 12; DB 142; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAAGATGATG 12
 111111111111

DB 94 CTGAAGATGATG 107

Search completed: August 2, 2001, 06:08:03
 Job time: 4.825 sec

us-09-479-862-6.rst

Thu Aug 2 10:27:00 2001

us-09-479-862-5.rng

Thu Aug 2 10:26:55 2001

XX Nucleic acids containing electron-transfer group, used as labels in
 PI hybridization assays, e.g., for denaturing, allowing repeat analyses on
 PI a single surface.
 XX Example 6; Page 127; 15pp; English.
 XX The present invention relates to a composition comprising two nucleic
 XX acids each containing an electron-transfer group (ETG) having
 XX different redox potentials. The invention is used for electrochemi-
 XX cally detecting nucleic acids, especially of substituted ones (mismatches)
 XX and single nucleotide polymorphisms, e.g., for denaturing,
 XX monitoring gene expression.
 XX Sequence 946 BP; 4 A; 144 C; 146 G; 147 A; 148 T; 149 C; 150 G; 151 A; 152 T; 153 C; 154 G; 155 A; 156 T; 157 C; 158 G; 159 A; 160 T; 161 C; 162 G; 163 A; 164 T; 165 C; 166 G; 167 A; 168 T; 169 C; 170 G; 171 A; 172 T; 173 C; 174 G; 175 A; 176 T; 177 C; 178 G; 179 A; 180 T; 181 C; 182 G; 183 A; 184 T; 185 C; 186 G; 187 A; 188 T; 189 C; 190 G; 191 A; 192 T; 193 C; 194 G; 195 A; 196 T; 197 C; 198 G; 199 A; 200 T; 201 C; 202 G; 203 A; 204 T; 205 C; 206 G; 207 A; 208 T; 209 C; 210 G; 211 A; 212 T; 213 C; 214 G; 215 A; 216 T; 217 C; 218 G; 219 A; 220 T; 221 C; 222 G; 223 A; 224 T; 225 C; 226 G; 227 A; 228 T; 229 C; 230 G; 231 A; 232 T; 233 C; 234 G; 235 A; 236 T; 237 C; 238 G; 239 A; 240 T; 241 C; 242 G; 243 A; 244 T; 245 C; 246 G; 247 A; 248 T; 249 C; 250 G; 251 A; 252 T; 253 C; 254 G; 255 A; 256 T; 257 C; 258 G; 259 A; 260 T; 261 C; 262 G; 263 A; 264 T; 265 C; 266 G; 267 A; 268 T; 269 C; 270 G; 271 A; 272 T; 273 C; 274 G; 275 A; 276 T; 277 C; 278 G; 279 A; 280 T; 281 C; 282 G; 283 A; 284 T; 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428 T; 429 C; 430 G; 431 A; 432 T; 433 C; 434 G; 435 A; 436 T; 437 C; 438 G; 439 A; 440 T; 441 C; 442 G; 443 A; 444 T; 445 C; 446 G; 447 A; 448 T; 449 C; 450 G; 451 A; 452 T; 453 C; 454 G; 455 A; 456 T; 457 C; 458 G; 459 A; 460 T; 461 C; 462 G; 463 A; 464 T; 465 C; 466 G; 467 A; 468 T; 469 C; 470 G; 471 A; 472 T; 473 C; 474 G; 475 A; 476 T; 477 C; 478 G; 479 A; 480 T; 481 C; 482 G; 483 A; 484 T; 485 C; 486 G; 487 A; 488 T; 489 C; 490 G; 491 A; 492 T; 493 C; 494 G; 495 A; 496 T; 497 C; 498 G; 499 A; 500 T; 501 C; 502 G; 503 A; 504 T; 505 C; 506 G; 507 A; 508 T; 509 C; 510 G; 511 A; 512 T; 513 C; 514 G; 515 A; 516 T; 517 C; 518 G; 519 A; 520 T; 521 C; 522 G; 523 A; 524 T; 525 C; 526 G; 527 A; 528 T; 529 C; 530 G; 531 A; 532 T; 533 C; 534 G; 535 A; 536 T; 537 C; 538 G; 539 A; 540 T; 541 C; 542 G; 543 A; 544 T; 545 C; 546 G; 547 A; 548 T; 549 C; 550 G; 551 A; 552 T; 553 C; 554 G; 555 A; 556 T; 557 C; 558 G; 559 A; 560 T; 561 C; 562 G; 563 A; 564 T; 565 C; 566 G; 567 A; 568 T; 569 C; 570 G; 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Thu Aug 2 10:27:04 2001

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

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DEFINITION	c769311 v1 NC1 CGAP Gas4 Homo sapiens cDNA clone IMAGE7624293 3' similar to SW-1118 HUMAN SLC1A3 TRIPLEX-BOX 13 ESTIMATED LENGTH 549 nt An repetitive element?? mRNA sequence.				
ACCESSION	AW151778				
VERSION	AW151778.1	GI:16199676			
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo;				
REFERENCE	1. (bases 1 to 549) NC1-CGAP http://www.ncbi.nlm.nih.gov/ncicgap/ .				
FEATURES	National Cancer Institute, Cancer Genome Anatomy Project (CGAP). Tumor Gene Index. Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: carbs@mail.nih.gov Tissue procurement: Christopher Miskulak, M.D., Ph.D.; Michael R. Emmert-Buck, M.D., Ph.D. cDNA library prepared by: Greiner Technology, Inc. cDNA Library Arrayed by: Greiner Technology, Inc. cDNA Sequencing by: Washington University Genome Sequencing Center cDNA Distribution by: NC1 CGAP clone distribution Information can be found through the L.M.A.G.E. Network (lmnet.adf.com) www.bioinformatics.cimacp.org/magene.html Seq primer: -40bp from above High quality sequence stop: 418. Location/Qualifiers 1..549 /organism "Homo sapiens" /db_xref "taxon:9606" /clone_1lb "IMAGE:2623293" /clone_1lb "NC1-CGAP_Gas4" /tissue_type "poorly differentiated adenocarcinoma with signet ring cell features" /lab_host "DB10B" /note="Organ: stomach; Vector: pCMV-Sport6; Site_1: SalI; Site_2: Not I; Cloned unidirectionally. Primer: oligo dT." Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"				
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ORIGIN					
	Query Match	24.6%	Score 544	DB 112	Length 549
	Best local Similarity	98.2%	Pred. No. 1, b: 64		
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DG	429	CTAGCTTGCAAAAAGAGAGAGACCTTTTAAACTCATTTTGAAGAGAGAGAGAGAAATG	370		
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DG	469	GGGATATAGATATAAATGTCACCTGTCAGAAAGAAAGAACTATCTATTAAGATTCAGGC	410		
QY	241	GGAGATAGGCTCAGAGCTCTTAATCTCAGAGCTTTTGGAGGCTTGAGAGCTGGTAGATCA	300		
DG	409	GGAGATAGGCTCAGAGCTCTTAATCTCAGAGCTTTTGGAGGCTTGAGAGCTGGTAGATCA	250		
QY	401	CACAGATCACAGCTTTCAGAGCTAGATGATGATCTTCAAGATCTTCAAGATCTTCAAGAA	460		
DG	249	CACAGATCACAGCTTTCAGAGCTAGATGATGATCTTCAAGATCTTCAAGATCTTCAAGAA	190		

Sequence version 4.5
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CM nucleic - nucleic search, using sw model

Run on: August 2, 2001, 07:12:41 : Search time 151.9 seconds
(without alignments)
2962.706 hits per cell updates/sec

Title: US-09-479-862-7
Percent score: 2167
Sequence: 1 GAAATGAAATGCTTTCATAA.....ATTATCAACAGCAATTATTAT 2167

Scoring table:
Gapop 10.0, Gapex 1.0

Searched: 424599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match OK
Maximum Match OK
Listing first 45 summaries

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6: 3022711 100 100 100 100 100 100 100 100 100 100

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

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2	2167	100.0	22234	3 US 08 884 424-7	Sequence 11, Appl 1
3	562.2	25.9	1120	4 US 08 884 424-7	Sequence 2, Appl 1
4	562.2	25.9	1120	4 US 08 884 424-7	Sequence 6, Appl 1
5	240	11.1	11464	4 US 08 884 424-7	Sequence 14, Appl 1
6	225.4	10.4	4715	4 US 09 085 199B-14	Sequence 44, Appl 1
7	221.2	10.2	246240	2 US 09 724 394A-20	Sequence 20, Appl 1
8	221.2	10.2	246240	2 US 08 724 394A-20	Sequence 2, Appl 1
9	221.2	10.2	246240	2 US 08 724 394A-20	Sequence 22, Appl 1
10	221	10.2	7735	2 US 08 687 080-115	Sequence 115, Appl 1
11	220.2	10.2	2743	3 US 08 417 747-1	Sequence 1, Appl 1
12	219.8	10.1	72928	3 US 09 009 914-1	Sequence 1, Appl 1
13	219	10.1	471	4 US 08 558 818-2	Sequence 2, Appl 1
14	219	10.1	471	4 US 08 974 469A-2	Sequence 2, Appl 1
15	219	10.1	471	4 US 08 832 189-2	Sequence 2, Appl 1
16	219	10.1	579	2 US 08 896 695A-7	Sequence 7, Appl 1
17	219	10.1	579	2 US 08 896 501A-5	Sequence 5, Appl 1
18	217.6	10.0	4773	3 US 08 884 324-9	Sequence 9, Appl 1
19	217.4	10.0	45060	4 US 08 814 095-7	Sequence 7, Appl 1
20	214.6	9.9	6769	1 US 08 480 784-20	Sequence 20, Appl 1
21	214.6	9.9	6769	1 US 08 484 553-20	Sequence 20, Appl 1
22	214.6	9.9	6769	1 US 08 487 002-20	Sequence 20, Appl 1
23	214.6	9.9	6769	1 US 08 484 554B-20	Sequence 20, Appl 1
24	214.6	9.9	6769	1 US 08 489 011B-20	Sequence 20, Appl 1
25	214.6	9.9	6769	4 US 08 850 727-20	Sequence 20, Appl 1
26	214.6	9.9	6769	5 US 08 850 727-20	Sequence 20, Appl 1
27	214.6	9.9	6769	5 US 08 850 727-20	Sequence 20, Appl 1

ALIGNMENTS

RESULT 1
US-08-884 424-7
Sequence 7, Application US/08884 424
Patent No. 6040286
GENERAL INFORMATION:
APPLICANT: TAKAKURA KOKORO
INVENTOR: KAKUJI TORIGOE
ATTORNEY: MITSUO FUKUMOTO
CLASSIFICATION: G06F 01/00, G06F 01/02, G06F 01/04, G06F 01/06, G06F 01/08, G06F 01/10, G06F 01/12, G06F 01/14, G06F 01/16, G06F 01/18, G06F 01/20, G06F 01/22, G06F 01/24, G06F 01/26, G06F 01/28, G06F 01/30, G06F 01/32, G06F 01/34, G06F 01/36, G06F 01/38, G06F 01/40, G06F 01/42, G06F 01/44, G06F 01/46, G06F 01/48, G06F 01/50, G06F 01/52, G06F 01/54, G06F 01/56, G06F 01/58, G06F 01/60, G06F 01/62, G06F 01/64, G06F 01/66, G06F 01/68, G06F 01/70, G06F 01/72, G06F 01/74, G06F 01/76, G06F 01/78, G06F 01/80, G06F 01/82, G06F 01/84, G06F 01/86, G06F 01/88, G06F 01/90, G06F 01/92, G06F 01/94, G06F 01/96, G06F 01/98, G06F 02/00, G06F 02/02, G06F 02/04, G06F 02/06, G06F 02/08, G06F 02/10, G06F 02/12, G06F 02/14, G06F 02/16, G06F 02/18, G06F 02/20, G06F 02/22, G06F 02/24, G06F 02/26, G06F 02/28, G06F 02/30, G06F 02/32, G06F 02/34, G06F 02/36, G06F 02/38, G06F 02/40, G06F 02/42, G06F 02/44, G06F 02/46, G06F 02/48, G06F 02/50, G06F 02/52, G06F 02/54, G06F 02/56, G06F 02/58, G06F 02/60, G06F 02/62, 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STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,707
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/074,448
FILING DATE: 09 JUN 1994
ATTORNEY/AGENT INFORMATION:
NAME: WOESSNER, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/AGENT NUMBER: 193,194 US 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-349-0431
TELEFAX: 612-349-4061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2743 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 194 human colon carcinoma cell line clone
FEATURE:
NAME/KEY: cJIS
LOCATION: 66..801
8-08 417-707-1


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1  APPLICANT: NAME: KASUSHIKI, KAISHA HAYASHIHARA SEIBUTSU KAGAKU
2  APPLICANT: KENKYUJO
3  APPLICANT: KENKAIDA, Toshiro
4  APPLICANT: TANIGUCHI, Mutsuko
5  APPLICANT: KONO, Kazuo
6  APPLICANT: KURIMOTO, Masashi
7  TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
8  TITLE OF INVENTION: WHICH INHIBITS INTERFERON PRODUCTION
9  NUMBER OF SEQUENCES: 9
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Browdy and Neimark
12 STREET: 419 Seventh Street N.W. Ste. 300
13 CITY: Washington
14 STATE: D.C.
15 COUNTRY: USA
16 ZIP: 20004
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC DOS/MS Dos
21 SOFTWARE: Word Perfect Version 5.0
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Browdy, Roger L.
24 REGISTRATION NUMBER: 25,619
25 REFERENCE/PACKET NUMBER: TORIGOE=1A
26 PRIORITY APPLICATION DATA:
27 PRIOR APPLICATION DATA: JP 58,240/95
28 FILING DATE: February 23, 1995
29 INFORMATION FOR SEQ ID NO: 1:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 471 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: double
34 TOPOLOGY: linear
35 MOLECULE TYPE: cDNA to mRNA
36 ORIGINAL SOURCE:
37 ORGANISM: human
38 INDIVIDUAL ISOLATE: liver
39 FEATURE:
40 NAME/KEY: mat peptide
41 LOCATION: 1..471
42 IDENTIFICATION METHOD: S
43 US-09-479-862-7

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Query Match: 10.1% Score 219; DB 4; Length 471;
 Best Local Similarity: 100.0%; Pred. No. 4,7e-32;
 Matches 253; Conservative 0; Mismatches 0; Indels 0; Gap 0

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14 RESULT 14
15 US-09-974-469A-2
16 Sequence 2: Application US/08974469A
17 Patent No. 6207641
18 GENERAL INFORMATION:
19 APPLICANT: KASUSHIKI KAISHA HAYASHIHARA SEIBUTSU KAGAKU
20 APPLICANT: KENKYUJO
21 APPLICANT: KIKIGAE, Kazuji
22 APPLICANT: TANIMOTO, Tadao
23 APPLICANT: FUKUDA, Shicharu
24 APPLICANT: KURIMOTO, Masashi
25 TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
26 NUMBER OF SEQUENCES: 9
27 CORRESPONDENCE ADDRESS:
28 ADDRESSEE: Browdy and Neimark
29 STREET: 419 Seventh Street N.W. Ste. 300
30 CITY: Washington
31 STATE: D.C.
32 COUNTRY: USA
33 ZIP: 20004
34 COMPUTER READABLE FORM:
35 MEDIUM TYPE: Floppy disk
36 COMPUTER: IBM PC compatible
37 OPERATING SYSTEM: PC DOS/MS Dos
38 SOFTWARE: Word Perfect Version 5.0
39 CURRENT APPLICATION DATA:
40 ATTORNEY/AGENT INFORMATION:
41 NAME: Browdy, Roger L.
42 REGISTRATION NUMBER: 25,618
43 REFERENCE/PACKET NUMBER: TORIGOE=1A
44 PRIORITY APPLICATION DATA:
45 PRIOR APPLICATION DATA: US/08974469A
46 FILING DATE:
47 APPLICATION NUMBER: US/08974469A
48 FILING DATE:
49 APPLICATION NUMBER: JP 78,457/95
50 FILING DATE: March 10, 1995
51 APPLICATION NUMBER: JP 274,989/95
52 FILING DATE: September 29, 1995
53 ATTORNEY/AGENT INFORMATION:
54 NAME: Browdy, Roger L.
55 REGISTRATION NUMBER: 25,618
56 REFERENCE/PACKET NUMBER: TORIGOE=1A
57 PRIORITY APPLICATION DATA:
58 PRIOR APPLICATION DATA: (202) 628-5197
59 TELEPHONE: (202) 747-3528
60 INFORMATION FOR SEQ ID NO: 2:
61 SEQUENCE CHARACTERISTICS:
62 LENGTH: 471 base pairs
63 TYPE: nucleic acid
64 STRANDEDNESS: double
65 TOPOLOGY: linear
66 MOLECULE TYPE: cDNA to mRNA
67 ORIGINAL SOURCE:
68 ORGANISM: human
69 INDIVIDUAL ISOLATE: liver
70 FEATURE:
71 NAME/KEY: mat peptide
72 LOCATION: 1..471
73 IDENTIFICATION METHOD: S
74 US-09-974-469A-2

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GenCore version 4.5
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OR nucleic acid sequence using a model

Run on: August 2, 2001, 05:01:54 : Search time 141.9 seconds
(without alignments)
168,249 hits (11,311 of dated/50,000)

Title: US-09-479-862-3
Perfect score: 135
Sequences: 1 AAGACGAGGAGGAGAGATTAGATGAGGAGGAGGAGG 135

Scoring table:
Gapop 10.0, Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 64138

Minimum DB seq length: 0
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Post-processing: Minimum Match: 0
Listing first 45 summaries

Database: Issued Patents, NA*
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2: 100.0 100.0 135 2 US-08-896-501A-5
3: 100.0 100.0 1120 4 US-08-884-424-2
4: 100.0 100.0 1120 4 US-08-884-424-6
5: 100.0 100.0 11464 4 US-08-884-424-1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1
US-08-884-424-3
Sequence 3, Application US/08884424
Patent No. 666263
GENERAL INFORMATION:
APPLICANT: TAKANORI OKURA
APPLICANT: KAKUJI TORIORE
TITLE: POLYMERIZATION OF A POLYMERIZABLE CATALYST
IN A POLYMERIZATION REACTION
INVENTOR: TAKANORI OKURA, KAKUJI TORIORE
ADDRESS: 419 SEVENTH STREET, N.W., SUITE 300
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA: 08-08-884-424
ATTORNEY/AGENT INFORMATION:
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT NUMBER: 3185, 007/96
REGISTERED NUMBER: 25,618
REGISTERED NUMBER: OKURA 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-6197
TELEFAX: 202-737-3528
TELEMAIL: 202-737-3528
SEQUENCE CHARACTERISTICS:
LENGTH: 135 base pairs
TYPE: nucleic acid
SYNTHESIS: double
TOPOLOGY: linear
STRUCTURE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placenta
FEATURE:
NAME KEY: 1.135
LOCATION: 1.135


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Query Match: 100.0% Score 15% DB 24 Length 579
Best Local Similarity 100.0% Prod No. 740-05
Matches 135: Conservative 0, Mismatches 0, Indels 0, Gaps 0

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      152  TGAAGCAAGATCTCTCTATGATCAACAGAAATGCGCTCTATTGCAATATGATG 211

      121  ATTGATGATGAGAG 145
      212  ATTGATGATGAGAG 226

RESULT 4
US-08-094-424-2
: Sequence 2, Application 05/0834124
: Patent No. 6060284
: GENERAL INFORMATION:
: APPLICANT: TAKANOJI KOKURA
: APPLICANT: KAKUJI TORIGOE
: APPLICANT: MASASHI KURIMOTO
: TITLE OF INVENTION: CIRCUIT FOR ESTIMATING A FINGERPRINT CAPABLE
: TITLE OF INVENTION: OF INCREASING THE PROBABILITY OF INTERFERING
: NUMBER OF SEQUENCES: 35
: CORRESPONDENT ADDRESS:
: ADDRESSEE: BROWDY AND NEWMARK
: STREET: 419 SEVENTH STREET, N.W., SUITE 300
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In License #1.0, Version #1.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 08/094-424
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 3F 185, 405/946
: FILING DATE: 27-JUN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, NEWMARK &
: REGISTRATION NUMBER: 25,618
: REFERENCE/PATENT NUMBER: OTHER 1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-8528
: INFORMATION FOR SEQ ID NO. 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1120 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: topology: linear
: FEATURE TYPE: CDS, mRNA
: HYPOTHEICAL: No
: ANTI-SENSE: No
: ORIGINAL SOURCE:
: ORGANISM: Human
: TISSUE TYPE: Liver
: FEATURE:
: NAME: CDS
: LOCATION: 1..177
: IDENTIFICATION METHOD: E
: NAME/FEAT: leader peptide
: LOCATION: 178..285
: IDENTIFICATION METHOD: S

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NAME/KEY: mail peptide
LOCATION: 286..756
IDENTIFICATION METHOD: S
NAME/KEY: VITER
LOC: 1..756
IDENTIFICATION METHOD: E
US 09 984 124-2

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Best local Similarity 100.0%, Pred. No. 9e+45;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gap 0;

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DB    269 AAAAACCTGAAATAGATAATATTGGG AAGTTGAATCAGAAATATCATGATCAAGTAAAGTAAAT
QY    61 TCAAGAGTAAGTTCCTGCATTTGATCGAAGAAGAAAATCGGTCTCTATTTCAGATATATGATATGAT
DB    329 GGAAGAGTAAGTTCCTGCATTTGATCGAAGAAGAAAATCGGTCTCTATTTCAGATATATGATATGAT
QY    121 ATTCTGACTGTAGAG 135
DB    389 ATTCTGACTGTAGAG 404

RESULT 5
US 09 842-160-6
Sequence 6; Application US/GB842180
Patent No. 6214584
SUBMITTER INFORMATION:
APPLICANT: KANISHIKI KAISUA HAYASHIMURA SEIRITSU KAKUKO
APPLICANT: KENKYUJO
APPLICANT: USHIO, Shimpei
APPLICANT: TORIGUCHI Kakuiji
APPLICANT: IANEMOTO, Tadao
APPLICANT: OKAMURA, Baraki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON PRODUCTION IMPROVING
NATURE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 14
CHECKED TYPE: ATFASTS:
ADDRESSEE: Growdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
CHECKER RELEASABLE FORM:
METHOD TYPE: Floppy disk
COMMENT: IBM PC compatible
TESTING SYSTEM: P-95/MS DOS
SOFTWARE: Word Perfect Version 5.0
CHECKER APPLICATION DATA:
APPLICATION NUMBER: 05/68/842,180
FILING DATE:
CLASSIFICATION:
PRIORITY INFORMATION:
APPLICATION NUMBER: 09/558,191
FILING DATE:
ACCEPTANCE NUMBER: JP 64,204,994
FILING DATE: No. 6214584-subst 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995
ADDRESS/AGENT INFORMATION:
NAME: Growdy, Kotet L.
REGISTRATION NUMBER: 25,618
REGISTERED AGENT NUMBER: USHIO I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEX: (202) 737 3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

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NAME/KEY: mail peptide
LOCATION: 246..756
IDENTIFICATION METHOD: S
NAME/KEY: VITER
LOCATION: 1..756
IDENTIFICATION METHOD: E
US 09 994 124-2

Query Match
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Matches 135; Conservative 0; Mismatches 0; Indels 0; Gap 0

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QY 121 ATTCTGATCTGAGAG 135
DB 389 ATTCTGATCTGAGAG 404

RESULT 5
US 09 942-160 6
Sequence 6; Application US/08042180
Patent No. 6214584
SUBMITTER INFORMATION:
APPLICANT: KANISHIKI KATSUO HAYASHIKAWA SEIJIUSO KATUKO
APPLICANT: KENKYUJO
APPLICANT: USHIO, Shimoda
APPLICANT: TORIGOE, Kakuji
APPLICANT: IANIMOTO, Tadao
APPLICANT: OKAMURA, Baraki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON PRODUCTION IMPROVING
NATURE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 14
CHECKED TYPE: AT+SS:
ADDRESSEE: Growdy and Naimark
STREET: 419 Seventh Street N.W. Ste. 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
CHECKER RELEASABLE FORM:
METHOD TYPE: Floppy disk
CHECKER: IBM PC compatible
CHECKER SYSTEM: PC 95/MS DOS
SOFTWARE: Word Perfect Version 5.0
CHECKER APPLICATION DATA:
APPLICATION NUMBER: 05/06/842,180
FILING DATE:
CLASSIFICATION:
PRIORITY INFORMATION:
APPLICATION NUMBER: 09/558,191
FILING DATE:
APPLICATION NUMBER: 21,054,204/94
FILING DATE: No. 6214584-subter 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995
APPLICANT/AGENT INFORMATION:
NAME: Growdy, Kotel L.
REGISTRATION NUMBER: 25,618
CHECKED BY: SEIT SUZUKI, USHIO I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

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us-09-479-862-3.rni

Thu Aug 2 10:26:50 2001

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?      IDENTIFICATION METHOD:
?      MS: 8-974-4694
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[illegible]

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: CATALAN SOURCE:
: ORGANISM: mouse
: LENSSE TYPE: Liver
: FEATURE:
: NAME/KEY: 1_471 mat peptide
: IDENTIFICATION METHOD: S
US-06 842 180 3

Query Match      38.1%   Score 51.4; DB 4; Length 471
Best local Similarity    79.9%; Prod. No. 5_4p 08)
Matches          9; Mismatches    3; Indels     2; Gap

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1 Sequence 6, Application US/09042180
2 Patent No. 6214584
3 GENERAL INFORMATION:
4 APPLICANT: KANSUKEI KAKIURA, KAKIURA, KAKIURA, KAKIURA, KAKIURA
5 APPLICANT: KENYUO
6 APPLICANT: USHIO, Shimpai
7 APPLICANT: TORIORE, Kakuji
8 APPLICANT: TANIMOTO, Taduo
9 APPLICANT: OKAMURA, Haruki
10 APPLICANT: KURIMOTO, Masashi
11 TITLE OF INVENTION: INTERFERON PRODUCTION METHOD
12 NUMBER OF SEQUENCES: 14
13 CORRESPONDENCE ADDRESS:
14 ADDRESS: Broadway and Newmark
15 STREET: 419 Seventh Street N.W., Ste. 400
16 CITY: Washington
17 STATE: D.C.
18 COUNTRY: USA
19 ZIP: 20004
20 COMPUTER RELEASABLE FORM:
21 MEDIUM TYPE: Floppy disk
22 COMPILER: IBM PC compatible
23 OPERATING SYSTEM: DOS/MS-DOS
24 SOFTWARE: Word Perfect Version 6.0
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/09042180
27 FILING DATE:
28 CLASSIFICATION:
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seq_documentation_block:
1 Sequence 1, Application US/09042180
2 Patent No. 6214584
3 GENERAL INFORMATION:
4 APPLICANT: KAKIURA, Haruki
5 APPLICANT: TANIMOTO, Taduo
6 APPLICANT: OKAMURA, Kakuji
7 APPLICANT: KURIMOTO, Masashi
8 APPLICANT: KAKIURA, Kakuji
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100 APPLICANT: KAKIURA, Kakuji

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253:  db_est 184: *
254:  db_est 185: *
255:  db_est 186: *
256:  db_est 187: *
257:  db_est 188: *
258:  db_est 189: *
259:  db_est 190: *

```

Prod. No. is the number of results produced by chance. A score greater than or equal to the score of the result to be tested and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search using sw model

Run on: August 2, 2001, 07:12:55 ; Search time 141.9 seconds
(with alignment)

US-09-479-862-5
Perfect score: 87
Sequence: 1 GAATAAGATGCTCTGAA.....CAATACGTTTATTATTATAG 87

Scoring table: IDENTITY_20C
Gapop 10.0 ; Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: 324599 seqs, 9465562 residues
2: 324599 seqs, 9465562 residues
3: 324599 seqs, 9465562 residues
4: 324599 seqs, 9465562 residues
5: 324599 seqs, 9465562 residues
6: 324599 seqs, 9465562 residues

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	87	100.0	87	US-08-884-324-5	Sequence 5, Appl
2	87	100.0	1120	US-08-884-324-5	Sequence 2, Appl
3	87	100.0	1120	US-08-884-324-5	Sequence 6, Appl
4	87	100.0	28994	US-08-884-324-5	Sequence 14, Appl
5	82	94.3	11464	US-08-884-324-5	Sequence 13, Appl
6	79	90.8	579	US-08-896-605A-7	Sequence 7, Appl
7	79	90.8	579	US-08-896-605A-7	Sequence 5, Appl
8	72	37.9	33	US-08-884-324-5	Sequence 23, Appl
9	33	37.9	33	US-08-884-324-5	Sequence 24, Appl
10	25.4	29.2	209	US-08-116-121-3	Sequence 3, Appl
11	25.2	29.0	5715	US-08-107-917-1	Sequence 1, Appl
12	24.4	28.0	3119	US-08-112-450-1	Sequence 7, Appl
13	24.4	28.0	8561	US-08-112-450-3	Sequence 3, Appl
14	24.2	27.9	862	US-08-817-260-1	Sequence 1, Appl
15	24	27.6	713	US-08-532-896-26	Sequence 26, Appl
16	23.8	27.4	1260	US-08-008-979A-3	Sequence 3, Appl
17	23.8	27.4	1260	US-08-460-618-4	Sequence 3, Appl
18	23.6	27.1	2310	US-08-956-182-14	Sequence 14, Appl
19	23.6	27.1	9171	US-08-032-592-5	Sequence 5, Appl
20	23.6	27.1	9171	US-08-302-832-5	Sequence 5, Appl
21	23.6	27.1	9171	US-08-530-198-5	Sequence 5, Appl
22	23.6	27.1	9171	US-08-469-883-5	Sequence 5, Appl
23	23.6	27.1	9171	US-08-738-170-5	Sequence 5, Appl
24	23.6	27.1	9171	US-08-617-697-5	Sequence 5, Appl
25	23.6	27.1	9171	US-08-719-641-5	Sequence 5, Appl
26	23.6	27.1	9171	US-08-038-692-6	Sequence 5, Appl
27	23.6	27.1	9171	US-08-302-932-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-884-324-5
Sequence 5, Application US/08884324
Patent No. 6060284
GENERAL INFORMATION:
APPLICANT: TAKAMOTO OKURA
ATTORNEY: KAKUJI TORIGOE
ADDRESS: 1-1-1, HONSHU, CHUO-KU, TOKYO, JAPAN
NUMBER OF SEQUENCES: 35
CURRENT APPLICATION DATA:
ADDRESS: 419 SEVENTH STREET, N.W., SUITE 300
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE: 27-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: ORU=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-638-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE: human
TISSUE TYPE: placenta
FEATURE:
NAME/KEY: cxon
LOCATION: 1..87

1 MOLECULE TYPE: cDNA to mRNA
2 HYPOTHETICAL: NO
3 ANTI-SENSE: NO
4 ORIGINAL SOURCE:
5 ORGANISM: human
6 TISSUE TYPE: liver
7 FEATURE:
8 NAME/KEY: 1-177 5'-UTR
9 IDENTIFICATION METHOD: S
10 FEATURE:
11 NAME/KEY: 178-285 leader peptide
12 IDENTIFICATION METHOD: S
13 FEATURE:
14 NAME/KEY: 286-756 mat peptide
15 IDENTIFICATION METHOD: S
16 FEATURE:
17 NAME/KEY: 757-1120 3'-UTR
18 IDENTIFICATION METHOD: S
19 US-09-842-180-46

Query Match 100.0% Score 87; DB 4; Length 1120;
Best Local Similarity 100.0% Pred. No. 1, 1e-21;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATAAAGATGGTGGTGAACACATAGAACACAAATTCATTCATTAAG 87
DB 170 GATAAAGATGGTGGTGAACACATAGAACACAAATTCATTCATTAAG 80
QY 61 TTATGCAATAGCTTATTCATTAAG 87
DB 230 TTATGCAATAGCTTATTCATTAAG 254

RESULT 4
US-09-842-324-14
Sequence 14, Application US-09-842-324
Patent No. 6060283
GENERAL INFORMATION:
APPLICANT: Takanoji KURA
APPLICANT: Kakuiji KORIJOE
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
OF INHIBITING THE PRODUCTION OF INTERFERON
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.00
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09-842-324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/AGENT NUMBER: GROUP 1
TELEPHONE: 202 628 5197
TELEFAX: 202 737 9528
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

1 LENGTH: 2894 base pairs
2 TYPE: nucleic acid
3 STRANDNESS: double
4 TOPOLOGY: linear
5 MOLECULE TYPE: Genomic DNA
6 ORIGINAL SOURCE:
7 ORGANISM: human
8 TISSUE TYPE: placenta
9 FEATURE:
10 NAME/KEY: 5'-UTR
11 LOCATION: 1..15606
12 IDENTIFICATION METHOD: E
13 NAME/KEY: leader peptide
14 LOCATION: 15607..15685
15 IDENTIFICATION METHOD: S
16 NAME/KEY: Intron
17 LOCATION: 15686..17056
18 IDENTIFICATION METHOD: E
19 NAME/KEY: leader peptide
20 LOCATION: 17057..17068
21 IDENTIFICATION METHOD: S
22 NAME/KEY: Intron
23 LOCATION: 17069..23451
24 IDENTIFICATION METHOD: E
25 NAME/KEY: leader peptide
26 LOCATION: 23452..20468
27 IDENTIFICATION METHOD: S
28 NAME/KEY: mat peptide
29 LOCATION: 20469..20586
30 IDENTIFICATION METHOD: S
31 NAME/KEY: Intron
32 LOCATION: 20587..21920
33 IDENTIFICATION METHOD: E
34 NAME/KEY: mat peptide
35 LOCATION: 21921..22054
36 IDENTIFICATION METHOD: S
37 NAME/KEY: Intron
38 LOCATION: 22055..26827
39 IDENTIFICATION METHOD: E
40 NAME/KEY: mat peptide
41 LOCATION: 26828..27046
42 IDENTIFICATION METHOD: S
43 NAME/KEY: 3'-UTR
44 LOCATION: 27047..28994
45 IDENTIFICATION METHOD: E
46 US-09-842-324-14

Query Match 100.0% Score 87; DB 4; Length 2894;
Best Local Similarity 100.0% Pred. No. 1, 1e-20;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATAAAGATGGTGGTGAACACATAGAACACAAATTCATTCATTAAG 87
DB 1559 GAATAAAGATGGTGGTGAACACATAGAACACAAATTCATTCATTAAG 1559
QY 61 TTATGCAATAGCTTATTCATTAAG 87
DB 15659 TTATGCAATAGCTTATTCATTAAG 15685

RESULT 5
US-09-842-324-14
Sequence 14, Application US-09-842-324
Patent No. 6060283
GENERAL INFORMATION:
APPLICANT: Takanoji KURA
APPLICANT: Kakuiji KORIJOE
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
OF INHIBITING THE PRODUCTION OF INTERFERON
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:

```

1  ACPRESSER:  DEWEY AND KUBARK
2  STREET:  419 Seventh Street, N.W., Suite 400
3  CITY:  Washington
4  STATE:  D.C.
5  COUNTRY:  USA
6  ZIP:  20004
7  COMPUTER READABLE FORM:
8  MEDIUM TYPE:  floppy disk
9  COMPUTER:  IBM PC compatible
10  OPERATING SYSTEM:  PC DOS/MS DOS
11  SOFTWARE:  Patent In Release #10, Version #1.0,
12  CURRENT APPLICATION DATA:
13  APLICALL IN NUMBER:  02/00/004, 624
14  FILING DATE:
15  CLASSIFICATION:  435
16  PRIOR APPLICATION DATA:
17  APPLICATION NUMBER:  JP 106, 437/86
18  FILING DATE:  27 JUN 1990
19  ATTORNEY/ADR:  INVENTOR:
20  NAME:  BOWEN, Robert L.
21  REGISTRATION NUMBER:  25,616
22  REFERENCE/SECRET NUMBER:  0000001
23  TELECOMMUNICATION INFORMATION:
24  TELEPHONE:  202 628-6197
25  TELEFAX:  202-787 6529
26  INFORMATION FOR SEQ ID NO: 15:
27  SEQUENCE CHARACTERISTICS:
28  LENGTH: 11464 base pairs
29  TYPE:  nucleic acid
30  STRANDEDNESS:  double
31  TOPOLOGY:  linear
32  Molecule TYPE:  genomic DNA
33  ORIGINAL SOURCE:
34  ORGANISM:  human
35  TISSUE TYPE:  placenta
36  FEATURE:
37  NAME/KEY:  5'UTR
38  LOCATION:  1..4
39  IDENTIFICATION METHOD:  E
40  NAME/KEY:  leader peptide
41  LOCATION:  4..62
42  IDENTIFICATION METHOD:  S
43  NAME/KEY:  147G
44  LOCATION:  83..1454
45  IDENTIFICATION METHOD:  E
46  NAME/KEY:  leader peptide
47  LOCATION:  1454..1465
48  IDENTIFICATION METHOD:  S
49  NAME/KEY:  147G
50  LOCATION:  1466..4848
51  IDENTIFICATION METHOD:  E
52  NAME/KEY:  leader peptide
53  LOCATION:  4849..4865
54  IDENTIFICATION METHOD:  S
55  NAME/KEY:  mat peptide
56  LOCATION:  4866..4983
57  IDENTIFICATION METHOD:  S
58  NAME/KEY:  intron
59  LOCATION:  4984..6317
60  IDENTIFICATION METHOD:  E
61  NAME/KEY:  5317-146
62  LOCATION:  6318..6451
63  IDENTIFICATION METHOD:  S
64  NAME/KEY:  147G
65  LOCATION:  6452..11224
66  IDENTIFICATION METHOD:  E
67  NAME/KEY:  mat peptide
68  LOCATION:  11225..11443
69  IDENTIFICATION METHOD:  S
70  NAME/KEY:  5'UTR
71  LOCATION:  11444..11464
72  IDENTIFICATION METHOD:  E
73  S 00 004 324-15

```

[illegible]

Country Match	90, 88;	Scores 79;	148;	Length 139;
Best Local (S.M.) 141; <td>100, 108; <td>Prod. No. 1, 89; <td>18; <td></td> </td></td></td>	100, 108; <td>Prod. No. 1, 89; <td>18; <td></td> </td></td>	Prod. No. 1, 89; <td>18; <td></td> </td>	18; <td></td>	
Match 79; <td>100, 108; <td>Prod. No. 1, 89; <td>18; <td></td> </td></td></td>	100, 108; <td>Prod. No. 1, 89; <td>18; <td></td> </td></td>	Prod. No. 1, 89; <td>18; <td></td> </td>	18; <td></td>	

QY 9 ATGGCTGCTGAGTAAAGAAATTCATCAATCTTGCGGAAAGAAATTTATGAC 68
 DB 1 AAGCTGTGTAAGTAAAGAAATTCATCAATCTTGCGGAAAGAAATTTATGAC 60

QY 69 AATAAGCTTACITATATAG 87
 DB 61 AATAAGCTTACITATATAG 79

RESULT 7
 US-08-896-501A-5
 : Sequence 5, Application US/08896501A
 : Patent No. 5991663
 : GENERAL INFORMATION:
 : APPLICANT: TANIMOTO, MASASHI
 : APPLICANT: KASUHI TORIGOE
 : TITLE OF INVENTION: GENETIC USA DROPPING A POLYPEPTIDE SEQUENCE
 : NUMBER OF SEQUENCES: 9
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROWDY AND NEWMARK
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20004
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: IBM PC compatible
 : SOFTWARE: Patent In Release #1.0, Version #1.00
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08896501A
 : FILING DATE: 18-JUL-1997
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: JP 213,267/1994
 : FILING DATE: 25-JUL-1996
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: JP 41,474/1997
 : FILING DATE: 31-JAN-1997
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BROWDY, ROGER L.
 : REGISTRATION NUMBER: 25,618
 : REFERENCE/DOCKET NUMBER: TANIMOTO 4
 : TELEPHONE: 202-628-5197
 : TELEFAX: 202-628-5197
 : INFORMATION FOR SEQ ID NO: 5:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 579 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA to mRNA
 : FEATURE:
 : NAME/KEY: leader peptide
 : LOCATION: 1..108
 : IDENTIFICATION METHOD: S
 : NAME/KEY: mat peptide
 : LOCATION: 109..579
 : IDENTIFICATION METHOD: S
 US-08-896-501A-5

Query Match 90.8%, Score 79, ID 2, Length 579
 Best Local Similarity 100.0%, Prod. No. 1,663,187
 Matches 79, Conservation 0, Mismatches 0, Labels 0, Gaps 0

QY 9 ATGGCTGCTGAGTAAAGAAATTCATCAATCTTGCGGAAAGAAATTTATGAC 68
 DB 1 AAGCTGTGTAAGTAAAGAAATTCATCAATCTTGCGGAAAGAAATTTATGAC 60

QY 69 AATAAGCTTACITATATAG 87
 DB 61 AATAAGCTTACITATATAG 79

DB 61 AATAAGCTTACITATATAG 79
 RESULT 8
 US-08-884-424-24
 : Sequence 24, Application US/08884424
 : Patent No. 6060284
 : GENERAL INFORMATION:
 : APPLICANT: TAKAMOTO, OKURA
 : APPLICANT: KASUHI TORIGOE
 : APPLICANT: MASASHI KURIMOTO
 : TITLE OF INVENTION: GENETIC USA DROPPING A POLYPEPTIDE SEQUENCE
 : NUMBER OF SEQUENCES: 35
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROWDY AND NEWMARK
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20004
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: IBM PC compatible
 : SOFTWARE: Patent In Release #1.0, Version #1.40
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08884424
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 3,347,377/96
 : FILING DATE: 27-JUN-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BROWDY, ROGER L.
 : REGISTRATION NUMBER: 25,618
 : REFERENCE/DOCKET NUMBER: GENA 1
 : TELEPHONE: 202-628-5197
 : TELEFAX: 202-628-5197
 : INFORMATION FOR SEQ ID NO: 24:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 33 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : BLASTABLE TYPE: cDNA
 US-08-884-424-24

Query Match 47.5%, Score 37, ID 3, Length 33
 Best Local Similarity 100.0%, Prod. No. 0,0044
 Matches 33, Conservation 0, Mismatches 0, Labels 0, Gaps 0

QY 41 CAACCTTGTGTAAGAAATTTATGACAAATAC 73
 DB 43 CAACCTTGTGTAAGAAATTTATGACAAATAC 1

RESULT 9
 US-08-884-424-24
 : Sequence 24, Application US/08884424
 : Patent No. 6060284
 : GENERAL INFORMATION:
 : APPLICANT: TAKAMOTO, OKURA
 : APPLICANT: KASUHI TORIGOE
 : APPLICANT: MASASHI KURIMOTO
 : TITLE OF INVENTION: GENETIC USA DROPPING A POLYPEPTIDE SEQUENCE
 : NUMBER OF SEQUENCES: 35
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROWDY AND NEWMARK
 : STREET: 419 Seventh Street, N.W., Suite 300

REGISTRATION NUMBER: 24, 35
REFERENCE/REFKIT NUMBER: 17200318

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TEL: FAX: (212) 382 0888

TELEFAX: (212) 482 0888
TELEFAX: 246925

TELEX: 246925

INFORMATION FOR SPQ ID NO: 26:

SEQUENCE CHARACTERISTICS

LENN: 713 base pair

1910-1911

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THE UNIVERSITY OF CHICAGO

BY THE COURT:

HYPERCALCAEMIA: N

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$$d^2 \mathcal{L} / d\alpha^2 = 2 \sum_{i=1}^n \frac{1}{\alpha^3} \left(\frac{1}{\alpha} - \frac{1}{\alpha_i} \right) \left(\frac{1}{\alpha} - \frac{1}{\alpha_i} \right) = 2 \sum_{i=1}^n \frac{1}{\alpha^3} \left(\frac{1}{\alpha} - \frac{1}{\alpha_i} \right)^2$$

\mathbf{f}_0	\mathbf{f}_1	\mathbf{f}_2	\mathbf{f}_3	\mathbf{f}_4	\mathbf{f}_5	\mathbf{f}_6	\mathbf{f}_7	\mathbf{f}_8	\mathbf{f}_9	\mathbf{f}_{10}	\mathbf{f}_{11}	\mathbf{f}_{12}	\mathbf{f}_{13}	\mathbf{f}_{14}	\mathbf{f}_{15}	\mathbf{f}_{16}	\mathbf{f}_{17}	\mathbf{f}_{18}	\mathbf{f}_{19}	\mathbf{f}_{20}	\mathbf{f}_{21}	\mathbf{f}_{22}	\mathbf{f}_{23}	\mathbf{f}_{24}	\mathbf{f}_{25}	\mathbf{f}_{26}	\mathbf{f}_{27}	\mathbf{f}_{28}	\mathbf{f}_{29}	\mathbf{f}_{30}	\mathbf{f}_{31}	\mathbf{f}_{32}	\mathbf{f}_{33}	\mathbf{f}_{34}	\mathbf{f}_{35}	\mathbf{f}_{36}	\mathbf{f}_{37}	\mathbf{f}_{38}	\mathbf{f}_{39}	\mathbf{f}_{40}	\mathbf{f}_{41}	\mathbf{f}_{42}	\mathbf{f}_{43}	\mathbf{f}_{44}	\mathbf{f}_{45}	\mathbf{f}_{46}	\mathbf{f}_{47}	\mathbf{f}_{48}	\mathbf{f}_{49}	\mathbf{f}_{50}	\mathbf{f}_{51}	\mathbf{f}_{52}	\mathbf{f}_{53}	\mathbf{f}_{54}	\mathbf{f}_{55}	\mathbf{f}_{56}	\mathbf{f}_{57}	\mathbf{f}_{58}	\mathbf{f}_{59}	\mathbf{f}_{60}	\mathbf{f}_{61}	\mathbf{f}_{62}	\mathbf{f}_{63}	\mathbf{f}_{64}	\mathbf{f}_{65}	\mathbf{f}_{66}	\mathbf{f}_{67}	\mathbf{f}_{68}	\mathbf{f}_{69}	\mathbf{f}_{70}	\mathbf{f}_{71}	\mathbf{f}_{72}	\mathbf{f}_{73}	\mathbf{f}_{74}	\mathbf{f}_{75}	\mathbf{f}_{76}	\mathbf{f}_{77}	\mathbf{f}_{78}	\mathbf{f}_{79}	\mathbf{f}_{80}	\mathbf{f}_{81}	\mathbf{f}_{82}	\mathbf{f}_{83}	\mathbf{f}_{84}	\mathbf{f}_{85}	\mathbf{f}_{86}	\mathbf{f}_{87}	\mathbf{f}_{88}	\mathbf{f}_{89}	\mathbf{f}_{90}	\mathbf{f}_{91}	\mathbf{f}_{92}	\mathbf{f}_{93}	\mathbf{f}_{94}	\mathbf{f}_{95}	\mathbf{f}_{96}	\mathbf{f}_{97}	\mathbf{f}_{98}	\mathbf{f}_{99}
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476 GCTGTTAATCAAATAAAAAATTGTAAAGAAATTAAGT

Searches completed: August 2, 2001, 00:12:40
 Job time: 746 sec.

Jobs time: 7846 sec.

GenCore version 4.5
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CM nucleotide - nucleotide search using sw model

Run on: August 2, 2001, 07:12:21 : Search time: 699.11 Seconds
(without alignments)
50,178 Million cell updates/sec

Title: US-09-479-862-6
Perfect score: 12
Sequence: 1-73AAGATGAG 12

Scoring table: IDENTITY_NUC
Gapop 10.0 / Gapext 1.0

Searched: 144157 seqs, 773074588 residues
Total number of hits satisfying chosen parameters: 2000414

Minimum db seq length: 0
Maximum db seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: GenBank: *

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98:	em_pi52:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result, kept in table, and is derived by analysis of the total score distribution.

SUMMARIES

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2	12	100.0	19	9	AP02040
3	12	100.0	20	9	AR056084
4	12	100.0	20	10	125425
5	12	100.0	25	9	AR059083
6	12	100.0	25	9	AR059145
7	12	100.0	25	10	125424
8	12	100.0	54	9	AX039045

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10	12	100.0	114	9	$\tilde{A}X(0, \gamma, 4, 2)$
11	12	100.0	114	9	$\tilde{A}X(0, \gamma, 4, 2)$
12	100.0	114	9	9	HS10A128
13	12	100.0	118	9	$\tilde{A}X(2, \gamma, 5)$
14	12	100.0	129	9	HS1A15135
15	12	100.0	134	9	$\tilde{A}X(1, 2, \gamma, 9)$
16	12	100.0	154	9	$\tilde{A}X(0, 1, 2, \gamma, 9)$
17	12	100.0	178	9	$\tilde{A}X(0, 1, 2, \gamma, 9)$
18	12	100.0	203	9	$\tilde{A}X(0, 1, 2, \gamma, 9)$
19	12	100.0	203	9	HSFA1A18
20	12	100.0	212	9	$\tilde{A}X(1, 0, 8, 8)$
21	12	100.0	224	9	$\tilde{A}X(2, 0, 9, 9)$
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25	12	100.0	249	9	$\tilde{A}X(0, 4, 9, 12)$
26	12	100.0	245	3	$\tilde{A}X(1, 4, 1, 3)$
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37	12	100.0	290	7	$\tilde{A}X(2, 4, 6, 117)$
38	12	100.0	300	8	$\tilde{A}X(2, 7, 5, 86)$
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CONCLUSIONS

[illegible]

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VERSION 125425.1 GI:1605294
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REFERENCE 1 (bases 1 to 25)
AUTHORS Mulder,C.
TITLE oligonucleotides with anti-Epstein-Barr virus activity
JOURNAL Patent: US 5550047 A 2 27-AUG-1996;
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VERSION AR059083.1 GI:5984660
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ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Mulder,C.
TITLE oligonucleotides with anti-Epstein-Barr virus activity
JOURNAL Patent: US 5847854 A 1 17-NOV-1999;
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DEFINITION Sequence 12 from Patent W0061768.
ACCESSION AR059145
VERSION AR059145.1 GI:1122842
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 54)
AUTHORS Graker,P., Rabenstein,M., Liu,B., Nowak,D. and Binnel,C.
TITLE Preparation of biologically active molecules
JOURNAL Patent: W0 0061768-A 12 19-01-2000;
GRAPE TIERRE (CH) ; ROBERTLEIN MUNAHEM (IL) ; ILL. BIOLOGICAL (US) ;

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DEFINITION Sequence 63 from patent US 5847854.
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VERSION AR059145.1 GI:5984722
KEYWORDS
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REFERENCE 1 (bases 1 to 25)
AUTHORS Mulder,C.
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ID 20 CTGAAGATGATG 9

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LOCUS AX059045
DEFINITION Sequence 12 from Patent W0061768.
ACCESSION AX059045
VERSION AX059045.1 GI:1122842
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 54)
AUTHORS Graker,P., Rabenstein,M., Liu,B., Nowak,D. and Binnel,C.
TITLE Preparation of biologically active molecules
JOURNAL Patent: W0 0061768-A 12 19-01-2000;
GRAPE TIERRE (CH) ; ROBERTLEIN MUNAHEM (IL) ; ILL. BIOLOGICAL (US) ;

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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Chordata;
    Mammalia; Primates; Catarrhini; Hominoidea; Homo.
  REFERENCE
    AUTHORS Graber, P., Robinson, M., Liu, B., Nozick, D., and Blumenthal, C.
    TITLE Preparation of biologically active molecules
    JOURNAL Patent, WO 0363768 A 9/19/01, 2000.
  GRABER, PIERRE (CHI) ; ROBINSON, MARGARETH (LI) ; LIU, BIANLING (LI) ;
  NOZICK, DANIELA (LI) ; YU, REN-WEI (LI) ; CHANG, CHANG (LI)
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    Mammalia; Primates; Catarrhini; Hominoidea; Homo.
  REFERENCE
    AUTHORS Bonville, P., Kessler, Montas, M.F., Almond, Respiration, L. Frades, C.,
    Naudin, L., Lemire, C., Burrel, N., Assmann, J., Post, S., Finkbe, B.,
    and Brewer, B.W.
    TITLE Nucleic acid and protein acids corresponding to human gene abel
    JOURNAL Patent, WO 0278076 A 30 28 Dec 2000.
  ACCESSION Pharm S.A. (PI)
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    Mammalia; Primates; Catarrhini; Hominoidea; Homo.
  REFERENCE
    AUTHORS Bachmann, R., Beckert, J., Wilkings, P., and Bickelmeier,
    U.
    TITLE Direct Submission
    JOURNAL Submitted (16 Oct 1995) The Sanger Centre, Hinxton, Cambridgeshire
    CB10 1BB, England. E-mail contact: hampshire@sanger.ac.uk
  2 (Gibson, 1 to 118)
  GIBSON, S.H., CHATHAM, A., NICHOL, A., and JORDAN, A.
  TITLE Identification of G-protein islands using a methylated DNA method.
  JOURNAL Nature, 373 (3), 246, 247 (1995)
  94282070
  COMMENT
    Vector: pETM 521(+)
    Clones are available from the UK MRC Human Genome Mapping Project
    Resource Centre, Hinxton, Cambridgeshire CB10 1BB, UK. See also
    1994-275884 and 1994-277107 for details
    of contact: biotech@compuserve.com
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  ACCESSION AX059912
  VERSION AX059912.1 GI:12405570
  KEYWORDS
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Chordata;
    Mammalia; Primates; Catarrhini; Hominoidea; Homo.
  REFERENCE
    AUTHORS Bonville, P., Kessler, Montas, M.F., Almond, Respiration, L. Frades, C.,
    Naudin, L., Lemire, C., Burrel, N., Assmann, J., Post, S., Finkbe, B.,
    and Brewer, B.W.
    TITLE Nucleic acid and protein acids corresponding to human gene abel
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CY 1 CTGAAGAAGAG 12
1111111111
DB 68 CTGAAGAAGAG 79

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DEFINITION Human SLS UT5087, c primer find, sequence tagged site.
ACCESSION U51026
VERSION 1.1
KEYWORDS SLS; PCR primer; SLS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetra-nucleotide repeat.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
1 (bases 1 to 178)
Gorkun, S.C., Matsunami, N., Plautko, R., Albertson, H., Ballarín, J., Melis, R., Lawrence, E., Boote, M., Boffa, R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elser, J., Linney, A., Linnell, J., M. and White, R.
Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome
Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@genome.med.utah.edu
Primer A: AACCTCAAGCTTACCTTAC
Primer B: ATTCTGAGGAGGCTCTT
End to Label: Primer B
pep Profile:
Initial Denaturation: 94° 400sec
Cycles Denaturation: Annealing Extension 94° 10 sec, 62° 10 sec, 72° 20 sec, 30
58° 10 sec, 72° 20 sec, 74° 10 sec
Gel: Acrylamide 7%, Formamide 42%, Urea 44%
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FEATURES
Source Location/Qualifiers
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Organization "Homo sapiens"
Zinc site "Zinc:9606"
Primer_bind complement (140..158)
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BASE COUNT 74 a 16 c 64 g 23 t 2 others
ORIGIN

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DB 151 CTGAAGAAGAG 162

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Search completed: August 2, 2001, 07:12:23
 Job time: 00:00 sec


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49 121 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
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RESULT 5
US-08-974-469A-2
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: Patent No. 6207641
: GENERAL INFORMATION:
: APPLICANT: KANISHI KEI KAISHA HAYASHIBARA SEIICHIRO KAKAKU
: ATTORNEY: KIKUYAMA
: APPLICANT: KIKUYAMA
: APPLICANT: TADAYOSHI TADA
: APPLICANT: FUKUDA, Shirohara
: APPLICANT: KURIMOTO, Masashi
: TITLE OF INVENTION: AGENT FOR GROWTH PROMOTION
: NUMBER OF SEQUENCES: 9
: CORRESPONDENT ADDRESS:
: ADDRESSEE: Broadway and Market
: STREET: 419 Seventh Street N.W., Ste. 400
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER RELEASABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS-DOS
: SOFTWARE: Word Perfect Version 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/974-469A
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/08/974-469A
: FILING DATE:
: APPLICATION NUMBER: JP 96-400000
: FILING DATE: March 10, 1995
: APPLICATION NUMBER: JP 274,988/95
: FILING DATE: September 29, 1995
: ATTORNEY/AGENT: THE SHIMIZU
: NAME: Broadway, Roder L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/ACKNOWLEDGMENT NUMBER: 00000000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 628-5197
: TELEFAX: (202) 337-4523
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 471 base pairs
: TYPE: nucleic acid
: STRANDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: ORIGINAL SOURCE:
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: LOCATION: 1..471
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US-08-974-469A-2

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Query Match 99.7% Score 133.64 DB 4: Length 471

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RESULT 6
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: GENERAL INFORMATION:
: APPLICANT: KANISHI KEI KAISHA HAYASHIBARA SEIICHIRO KAKAKU
: ATTORNEY: KIKUYAMA
: APPLICANT: KIKUYAMA
: APPLICANT: TADAYOSHI TADA
: APPLICANT: FUKUDA, Shirohara
: APPLICANT: KURIMOTO, Masashi
: TITLE OF INVENTION: AGENT FOR GROWTH PROMOTION
: NUMBER OF SEQUENCES: 14
: CORRESPONDENT ADDRESS:
: ADDRESSEE: Broadway and Market
: STREET: 419 Seventh Street N.W., Ste. 400
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER RELEASABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS-DOS
: SOFTWARE: Word Perfect Version 5.0
: CURRENT APPLICATION DATA:
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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/08/942-180
: FILING DATE:
: APPLICATION NUMBER: JP 954,283/94
: FILING DATE: No. 6214584-sub 19, 1994
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 628-5197
: TELEFAX: (202) 337-4523
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 471 base pairs
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: TOPOLOGY: linear
US-08-942-180-2

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Query Match 99.7% Score 133.64 DB 4: Length 471

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RESULT 14
US-09-479-862-4
Sequence 6, Application US/09/4449A
Patent No. 6,197,297
GENERAL INFORMATION:
APPLICANT: 9999 FARMER, FARMER, FARMER, FARMER, FARMER, FARMER
APPLICANT: KERRYJO
APPLICANT: KUNIKATA, Yoshio
APPLICANT: TANGGUL, Matsuko
APPLICANT: KOHNO, Koizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: METHOD FOR PRODUCING A POLYMER
TITLE OF INVENTION: METHOD FOR PRODUCING A POLYMER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown and Nemark
STREET: 419 Seventh Street N.W., Ste. 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS/Windows
SOFTWARE: Word Perfect Version 5.0
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Robert L.
REGISTRATION NUMBER: 25,018
REFERENCE/DOCKET NUMBER: FELT-1

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Query Match: 56.4% Score 75.6; DB 4; Length 471;
Best Local Similarity: 72.7% Prod. No. 6,96,162
Matches: 96; Conserved: 1; Mismatch: 45; Index: 6; Gap: 0;
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DB 118 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 177
QY 63 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 122
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RESULT 14
US-09-479-862-4
Sequence 6, Application US/09/4449A
Patent No. 6,197,297
GENERAL INFORMATION:
APPLICANT: 9999 FARMER, FARMER, FARMER, FARMER, FARMER, FARMER
APPLICANT: KERRYJO
APPLICANT: KUNIKATA, Yoshio
APPLICANT: TANGGUL, Matsuko
APPLICANT: KOHNO, Koizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: METHOD FOR PRODUCING A POLYMER
TITLE OF INVENTION: METHOD FOR PRODUCING A POLYMER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown and Nemark
STREET: 419 Seventh Street N.W., Ste. 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS/Windows
SOFTWARE: Word Perfect Version 5.0
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Robert L.
REGISTRATION NUMBER: 25,018
REFERENCE/DOCKET NUMBER: FELT-1

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FROM APPLICATION DATA: 02/09/99, 979
 FILING DATE: 02/09/99, 979
 APPLICATION NUMBER: JP 79,437,995
 FILING DATE: March 10, 1995
 APPLICATION NUMBER: JP 274,988/95
 FILING DATE: September 29, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Browdy, Knight L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/SECRET NUMBER: PERDUE 1A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-5197
 TELEFAX: (202) 737-5538
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 471 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:
 ORGANISM: mouse
 INDIVIDUAL ISOLATE: liver
 FEATURE:
 NAME/KEY: mat peptide
 LOCATION: 1..471
 IDENTIFICATION METHOD: S
 US-09-479-862-4

Query Match: 56.4% Score 75.6; DB 4; Length 471;
 Best Local Similarity: 72.7% Prod. No. 6, no-16;
 Matches: 96; Conservative: 1; Mismatches: 35; Indels: 0; Gaps: 0;
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RESULT 15
 US-09-479-862-4
 Sequence 3, Application US/0947180
 Patent No. 6214584
 GENERAL INFORMATION:
 APPLICANT: KANISHI, KAZUO KANISHI, KAZUO KANISHI, KAZUO
 APPLICANT: KENYUJO
 APPLICANT: USHIO, Shunpei
 APPLICANT: TORIGOE, Kakuji
 APPLICANT: TANIMOTO, Tadao
 APPLICANT: OKAMURA, Haruki
 APPLICANT: KURIMOTO, Masashi
 TITLE OF INVENTION: INTERFERON PROTEIN INHIBITOR
 TITLE OF INVENTION: POLYPEPTIDE
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Browdy and Knight L.
 STREET: 419 Seventh Street N.W. Ste. 400
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS-DOS
 CURRENT APPLICATION DATA:
 FILING DATE: 02/09/99, 979
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 02/09/99, 979
 FILING DATE: 02/09/99, 979
 APPLICATION NUMBER: JP 401,234/94
 FILING DATE: N/A 6214584 number 16, 1994
 APPLICATION NUMBER: 10048102
 FILING DATE: September 18, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Browdy, Knight L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/SECRET NUMBER: USHIO 1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-5197
 TELEFAX: (202) 737-5528
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 471 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:
 ORGANISM: mouse
 INDIVIDUAL ISOLATE: liver
 FEATURE:
 NAME/KEY: 1..471 mat peptide
 IDENTIFICATION METHOD: S
 US-09-479-862-4

Query Match: 56.4% Score 75.6; DB 4; Length 471;
 Best Local Similarity: 72.7% Prod. No. 6, no-16;
 Matches: 96; Conservative: 1; Mismatches: 35; Indels: 0; Gaps: 0;
 QY 3 AATGACCCGAGCAATATTTATTATTAAGTATGATTAAGATACAGAGGATAGGATG 62
 DB 118 AGTGAATCCGAGCAATATTTATTATTAAGTATGATTAAGATACAGAGGATG 177
 QY 63 GTCGTAACGATGCTCTGTCGCAAGGTCGAGAAATTTCAATCTCTCTCTGAGAA 122
 DB 178 GCTGACGAGCTCTCTGTCGCAAGGTCGAGAAATTTCAATCTCTCTCTGAGAA 247
 QY 123 ATTTCCTTTAA 144
 DB 248 ATTTCCTTTAG 249

Search completed: August 2, 2001, 07:12:36
 Job time: 784.2 sec

Genome version 4.5
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Molecule nucleic search, using sw model

Run on: August 2, 2001, 07:11:39 : Search time: 699.11 seconds
(without alignments)
64,789 Million cell updates/sec

Title: US 09-479-862-5
Perfect score: 87

Sequence: 1 GAAATAAGATGAGTTCAGAACAAGAAAGTTCATCTTATAG 87

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 184157 seqs, 773874592 residues

Total number of hits satisfying chosen parameters: 2008414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: GenEmbl: *

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4:	qb_ba4:*
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56: qb_s9:*

57: qb_un:*

58: qb_v1:*

59: qb_v12:*

60: qb_h0q1:*

61: qb_h0q2:*

62: qb_h0q3:*

63: qb_h0q4:*

64: qb_h0q5:*

65: qb_h0q6:*

66: qb_h0q7:*

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93: qb_pr9:*

94: qb_r01:*

95: qb_r02:*

96: qb_r04:*

97: qb_r10:*

98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query			Descript	
	No.	Score	Match Length DB ID		
1	87	100.0	87 10	E15644	E15644 Homo sapien
2	87	100.0	1102 91	D49950	D49950 Homo sapien
3	87	100.0	1120 10	E14759	E14759 Homo sapien
4	87	100.0	1120 10	E15641	E15641 Homo sapien
5	87	100.0	1120 45	E11745	E11745 Homo sapien
6	87	100.0	28994 10	E15653	E15653 Homo sapien
7	87	100.0	164655 83	AB002884	AB002884 Homo sapien
8	87	100.0	167065 73	AB002883	AB002883 Homo sapien

C	87	100.0	122859	61	AC010815	AC010815 Homo sapi	
10	87	100.0	187516	61	AC006648	AC006648 Homo sapi	
11	82	94.3	11464	10	E15652	E15652 Human gene	
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13	79	90.8	579	9	AK006452	AK006452 Sequence	
14	79	90.8	579	10	E15693	E15693 cDNA clone	
15	79	90.8	582	5	AK006456	AK006456 Sequence	
16	79	90.8	589	88	AF077641	AF077641 Homo sapi	
17	76	87.4	579	97	BS000434	BS000434 Human inter	
18	74.2	85.3	623	89	AF033732	AF033732 Macaca mu	
19	74.2	85.3	773	7	U0401043	U0401043 ovine arle	
20	69.4	79.8	754	7	AF124789	AF124789 Bos tauru	
C	21	69.4	79.8	145682	71	AC004093	AC004093 Homo sapi
C	22	69.4	79.8	224793	68	AC024942	AC024942 Homo sapi
23	66.2	76.1	582	7	E0101F	E0101F Equus cabal	
24	66.2	76.1	582	5	AK011258	AK011258 Sequence	
25	60	69.0	659	9	AK009043	AK009043 Sequence	
26	59.8	68.7	582	7	E1513F	E1513 cDNA clone	
27	59.8	68.7	582	7	AK011258	AK011258 Sequence	
28	59.8	68.7	579	7	E0101F	E0101F Equus cabal	
29	54.8	61.8	712	7	AF046211	AF046211 Felis cat	
30	52.2	60.0	579	7	AF151088	AF151088 Sus scro	
31	52.2	60.0	600	7	AF176949	AF176949 Sus scro	
32	52.2	60.0	600	7	SS004701	SS004701 Sus scro	
33	52.2	60.0	665	7	AF010093	AF010093 Sus scro	
34	47.6	54.7	628	95	BN006244	BN006244 Rattus nor	
35	45	51.7	572	94	BM006244	BM006244 Mus musculu	
36	45	51.7	866	94	BS000434	BS000434 Homo sapi	
37	45	51.7	110931	76	AK024709	AK024709 Mus muscu	
38	44.4	51.0	665	95	BN077777	BN077777 Rattus norv	
39	44.4	51.0	722	95	BN077776	BN077776 Rattus norv	
40	49	44.8	75	9	AK009042	AK009042 Sequence	
41	31.6	46.3	555	97	BM006244	BM006244 Homo sapi	
42	31.6	46.3	90458	81	AL513459	AL513459 Homo sapi	
43	31.6	46.3	155343	90	AL465361	AL465361 Human DNA	
C	44	31.6	36.3	188964	69	AC025151	AC025151 Homo sapi
C	45	31.2	35.9	175606	87	AC011604	AC011604 Homo sapi

RES0011

1

AL1389815

RES0011	E15644	E15644	87 bp	DNA	PA1	28 JUL 1999
LOCUS	An exon of human gene for inter-tetrah gamma-inducing protein.					
DEFINITION	E15644					
ACCESSION	E15644.1 (31,573)327					
VERSION	ip_199909099-A/4					
FEATURES	Homo sapiens					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	Eickbush et al; Mol Cell Biol 1997; 17(12):3777-3782					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
TITLE	1. (bases 1 to 87)					
JOURNAL	Chrom Res 1999; 5(1):1-12					
COMMENT	CHROMOSOMAL DNA CLONING FOR IDENTIFYING THE HUMAN PROTEIN-11					
	HAYASHI et al; Jpn J Cancer Res 1998; 89(1):1-12					
	HAYASHI et al; Jpn J Cancer Res 1998; 89(1):1-12					
	HAYASHI et al; Jpn J Cancer Res 1998; 89(1):1-12					
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	HAYASHI et					

ALIGNMENTS

RESULT	1
E15644	
LOCUS	E15644 87 bp DNA 28 JUL 1999
DEFINITION	An exon of human gene for interferon gamma-inducing protein.
ACCESSION	E15644
VERSION	E15644.1 01-07-1997
KEYWORDS	bp 100000000-000000000
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Primates; Hominoidea; Hominidae; Homo; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo; (bases 1 to 87)
REFERENCE	Okada, T., Fujisaki, K., and Kunitada, M.
AUTHORS	Okada, T., Fujisaki, K., and Kunitada, M.
TITLE	CHROMOSOMAL DNA CLONING FOR IDENTIFYING THE INDUCING PRODUCTION OF INTERFERON GAMMA IN TUBERCULOSIS-PRONE PATIENTS
JOURNAL	Journal of Interferon Research, Vol. 17, No. 1, 1997, pp. 1-5
COMMENT	1. (bases 1 to 87) 2. (bases 1 to 1102) 3. (bases 1 to 1102) 4. (bases 1 to 1102) 5. (bases 1 to 1102) 6. (bases 1 to 1102) 7. (bases 1 to 1102) 8. (bases 1 to 1102) 9. (bases 1 to 1102) 10. (bases 1 to 1102) 11. (bases 1 to 1102) 12. (bases 1 to 1102) 13. (bases 1 to 1102) 14. (bases 1 to 1102) 15. (bases 1 to 1102) 16. (bases 1 to 1102) 17. (bases 1 to 1102) 18. (bases 1 to 1102) 19. (bases 1 to 1102) 20. (bases 1 to 1102) 21. (bases 1 to 1102) 22. (bases 1 to 1102) 23. (bases 1 to 1102) 24. (bases 1 to 1102) 25. (bases 1 to 1102) 26. (bases 1 to 1102) 27. (bases 1 to 1102) 28. (bases 1 to 1102) 29. (bases 1 to 1102) 30. (bases 1 to 1102) 31. (bases 1 to 1102) 32. (bases 1 to 1102) 33. (bases 1 to 1102) 34. (bases 1 to 1102) 35. (bases 1 to 1102) 36. (bases 1 to 1102) 37. (bases 1 to 1102) 38. (bases 1 to 1102) 39. (bases 1 to 1102) 40. (bases 1 to 1102) 41. (bases 1 to 1102) 42. (bases 1 to 1102) 43. (bases 1 to 1102) 44. (bases 1 to 1102) 45. (bases 1 to 1102)

[illegible][illegible]

|||||
26909 AAGAGGAAATTTGAACTCTAATGATACGAGAGAAATTTCTAGCTTGGA 26958
128 uLysGluArgAspGluPheGlyLeuLysLysGluAspGluLeu 145
|||||
26959 AAGAGAGAGAGAGCTTTTAAATCTATTTTGAAGAGAGAGAGAGAGAGAG 27008
145 LysAspArgSerPheMetPheThrValGluAsnGluAsp 157
|||||
27009 GAGATAGATCTATAATGCTTATGTTTCAAAAGAGAGAG 27046

SEARCH REQUEST FORM

Scientific and Technical Information Center

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 Art Unit _____ Phone Number 30 _____ Serial Number: _____
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If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher <u>Toby Port</u>	NA Sequence (#) <u>6</u>	STN _____
Searcher Phone # <u>308-3531</u>	AA Sequence (#) _____	Dialog _____
Searcher Location _____	Structure (#) _____	Questel Orbit _____
Date Searcher Picked Up <u>8/1</u>	Bibliographic _____	Dr Link _____
Date Completed <u>8/3</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time <u>10</u>	Fulltext _____	Sequence Systems <u>cg</u>
Clerical Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time <u>10</u>	Other _____	Other (specify) _____

The first part of the paper discusses the importance of the study of the history of the United States. It is argued that the study of the history of the United States is essential for a full understanding of the country and its people. The second part of the paper discusses the importance of the study of the history of the world. It is argued that the study of the history of the world is essential for a full understanding of the world and its people. The third part of the paper discusses the importance of the study of the history of the United States and the world. It is argued that the study of the history of the United States and the world is essential for a full understanding of the United States and the world.